

Db 383 AATATTGGCATTGAAGGCTTTAAAGGCAATGATAGTAAAGATGCTAAAGATACAC 442
 Qy 457 ACACACGGGGCTGAGCGGCAATCTAGAGTCAAGTGAAGACCCGCTTATGTGAACT 516
 Db 443 TCATACAAAGAGAGAGAGGAAATTTCTGAGAGAGATGAAGATCCCTTATGTGATTT 502
 Qy 517 GGCCTATGCTTCCAGACTGGTGGCAAACTCATCTCATCTTGAAGTGGCTCAGTGGT 576
 Db 503 AATTATCTCTTCACTGGTGGAAACTTCACTCATCTTGAAGTGGCTCAGTGGAG 562
 Qy 577 CGAGCTCTTCAAGCATCTGAGAGGAGGAGGATCTTCCGGAAGTACGGCTGCTTCA 636
 Db 563 AGAATATTATTATGACAGTGAAGAGAGGATATTATGAAGACACTGCTGCTTTTA 622
 Qy 637 CTTGGCAGAAATCTTCATGCGCTTTGGGCAATTCATCAAAAGGAGATCATCTACAG 682
 Db 623 CTTGGCAGAAATCTTCATGCGCTTTGGGCAATTCATCAAAAGGAGATCATCTACAG 682
 Qy 697 CCTCAAGCCGAGAACATCATGCTCAGACGCGGCGCATCAAACTGACCGACTTTGG 756
 Db 683 CCTGAAGCCGAGAAATCATGCTTATATCACCAGGTGATGAAGTGAAGACTTTGG 742
 Qy 757 ACTCTGCAAGAGTCTATCATGAGAGGCGGCTCCTCATCAGCTTCTGCGGCACTTGA 816
 Db 743 ACTATGCAAAAGATCTATCATGATGAAACATCAGACACATTTTGTGGAACAATGA 802
 Qy 817 GTACATGCGCCCTGAGATCTGTGGCGAGGCGCAACCGGGGGTGGAGTGGAGG 876
 Db 803 ATACTTGGCCCTGAAATCTTATGATGAGAGTGGCCAAATGCTGCTGATGGTGGAG 862
 Qy 877 CTTGGGCGCCCTGATGATGACATGCTCATGATGCGCGCTTACCGAGAGAACCG 936
 Db 863 TTTGGAGCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 922
 Qy 937 GAAAGAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 996
 Db 933 AAGAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 982
 Qy 997 AGATGCGCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1056
 Db 983 AGAAGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1042
 Qy 1057 TGGCCAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1116
 Db 1043 TGGTCTGCGGAGCTGAGGAGAGTTCAGAGCTCATCTTGAAGCATTAATGAGGA 1102
 Qy 1117 CGACTTCTGCGCTGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1176
 Db 1103 AGAAGCTTCTGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1162
 Qy 1177 CGTGAAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1236
 Db 1163 TGTAAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1222
 Qy 1237 AGCCCTCAGCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1296
 Db 1223 AACTCTCAGTGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1282
 Qy 1297 CCTGAGACATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1356
 Db 1283 ACTTGAAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1342
 Qy 1357 CAAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1407
 Db 1343 TATTGGCAGCGAGAGACCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1393

RESULT 14
 AX333655
 LOCUS AX333655 2346 bp DNA linear PAT 09-JAN-2002
 DEFINITION Sequence 4164 from Patent WO0194629.
 ACCESSION AX333655

VERSION AX333655.1 GI:18124374
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horvitz, S., Soppet, D.R. and Weaver, Z.
 Cancer gene determination and therapeutic screening using signature gene sets
 JOURNAL Patent: WO 0194629-A 4164 13-DEC-2001;
 FEATURES
 source
 location/Qualifiers
 1..2346
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 750 a 453 c 558 g 585 t
 ORIGIN
 Query Match 34.1%; Score 619.8; DB 6; Length 2346;
 Best Local Similarity 70.5%; Pred. No. 7.8e-115;
 Matches 824; Conservative 0; Mismatches 344; Indels 0; Gaps 0;
 Qy 240 TGGGCACTATGAGAGGCTGAGTGAAGCAGCGGTGAGCGTGGCCAGAGCGCA 299
 Db 224 TGAACATTTGAGAAATTTGAAATCTCAGAAATAGTGTGAACAGAGGCGCAAAAAA 283
 Qy 300 TGGGCGCCCATGCTTTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 359
 Db 284 TCAGACCAAGAAATTTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 343
 Qy 360 TCCAGTGGGAAAGGTGACAGGAGCAGCACTTGGGCAAAATATATGATGAAAGTCTTA 419
 Db 344 TTCAAGTACGAAATATTAACAGAGCAAAATCTGAGAAATATTTGCTAGAAAGTGTGA 403
 Qy 420 GGAAGCCAAATTTGTGGCAATGCGCAAGACAGACACACAGAGGCTGAGCGAACA 479
 Db 404 AAGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 463
 Qy 480 TTCTAGAGTGAAGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 539
 Db 464 TTCTGAGAGAAATGAGAGCAATGCTGATGATGATGATGATGATGATGATGATGATGATG 523
 Qy 540 GCAAACTTACTCATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 599
 Db 524 GAAAACTTACTCATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 583
 Qy 600 GAGAGGAGATCTTCTGAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 659
 Db 584 GAGAGGAGATTTATGAGG 643
 Qy 660 TGGGCAATCTCAGTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 719
 Db 644 TGGGCAATTTATCAATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 703
 Qy 720 TCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 779
 Db 704 TTAACTACCAAGGTATGTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 763
 Qy 780 AAGGCGCGTCACTCACTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 839
 Db 764 ATGGAAGGTGACACACACATTTTGTGAACAATGAAATGATGAGGAGGAGGAGGAGGAGG 823
 Qy 840 TGGGCAATGAGCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 899
 Db 824 TGAGAAAGTGGCCACAAATGCTGTGATGATGATGATGATGATGATGATGATGATGATG 883
 Qy 900 TGGTCACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 959
 Db 884 TGGTCACTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 943
 Qy 960 TCAGGGGAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1019

Qy	1529	AAGTCCAAAGAGGGGGCGGTGGGGGTCCAGGGGCGCTGAGAAAGCGGGTGGGGGTGAAGGTAG	1588
Db	1449	AAGTCCAAAGAGGGGGCGGTGGGGGTCCAGGGGCGCTGAGAAAGCGGGTGGGGGTGAAGGTAG	1508
Qy	1389	CCCTTGAACCCCTTCCCTCGCGCTGTGAGACGACGACCTGGGCGCATGTTCCAGAGAC	1648
Db	1509	CCCTTGAACCCCTTCCCTCGCGCTGTGAGAGGACGACGACCTGGGCGCATGTTCCAGAGAC	1568
Qy	1649	CTGGGGGTGTGTCTGGAGGGGGGGGTGTGAGTCCGATGAAATGTGTCTCTCTGGGGCA	1708
Db	1569	CTGGGGGTGTGTCTGGGGGTGTGAGTCCGATGAAATGTGTCTCTCTGGGGCA	1628
Qy	1709	GCTGTGCCCCCTGAATCATATGGGCAAGGAGGCGCCCGCACACCCCGGCTCAACTGCTC	1768
Db	1629	GCTGTGCCCCCTGAATCATATGGGCAAGGAGGCGCCCGCACACCCCGGCTCAACTGCTC	1688
Qy	1769	CCGTGGAAGATTAAGGGCGGAATCATGTGAAAAAAAAAAAAAAAAAAAAA	1812
Db	1689	CCGTGGAAGATTAAGGGCGGAATCATGTGAAAAAAAAAAAAAAAAAAAAA	1732

RESULT 2
 US-08-966-316-10
 ; Sequence 10 Application US/08966316
 ; Patent No. 5932445
 ; GENERAL INFORMATION:
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Reddy, Roopa
 ; APPLICANT: Murthy, Lynn E.
 ; APPLICANT: Mathur, Preete
 ; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/966,316
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PR-0424 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1637 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: SKINBIT01
 ; CLONE: 1869688
 ; US-08-966-316-10

Query Match 60.8%; Score 1104.4; DB 2; Length.16377
 Best Local Similarity 98.8%; Pred. No. 1.2e-248;

```

QY 1175 GACGTGAGCCAGTTTGATACCCGCTTCACACGGCAGACGCGGTGGACAGTCTGATGAC 1234
      |||||||
Db 1254 GAGGTGAG-CAGTTGATACCGCTTCACACGGCAGACGCGGTGGACAGTCTGATGAC 1312
QY 1235 ACAGCCCTTAGGAGAGAGTCCCAACAGGCGCTTCCTGGGCTTCATATAGTGGCCCGCTCT 1294
      |||||
Db 1313 ACAG-CCTTAGGAGAGAGTCCCAACAGGCGCTTCCTGGGCTT-ACATTAAGTGGCGC-GTCT 1369
QY 1295 GTCTGTGACAG 1305
      |||||||
Db 1370 GTCTGTGACAG 1380

RESULT 3
US-08-749-902-4
: Sequence 4, Application US/08749902
: Patent No. 5985635
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Goli, Surya K.
: APPLICANT: Hillman, Jennifer L.
: TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
: TITLE OF INVENTION: PROTEIN KINASES
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: US
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08749,902
: FILING DATE: Filed Herewith
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0150 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1607 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: CLONE: Consensus
US-08-749-902-4

Query Match 39.6%; Score 720; DB 2; Length 1607;
Best Local Similarity 99.1%; Pred. No. 5.5e-159;
Matches 734; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 874 GAGCCTGGGGCCCTGATGTACGACATCTCATCGATCGCCGCCCTTATCCGCAGAGAA 933
      |||||||
Db 868 GGGCGTGGGACCGCTGATGTACGACATCTCATCGATCGCCGCCCTTATCCGCAGAGAA 927
QY 934 CCGGAAGAAAACCATGATTAAGATCATCAGGGGCAAGCTGGCACTGCCCTTACTCTCAC 993
      |||||||
Db 928 CCGGAAGAAAACCATGATTAAGATCATCAGGGGCAAGCTGGCACTGCCCTTACTCTCAC 987
QY 994 CCCAATGCCCGGAGACCTGTTCACAAAATTTCTGTAAGACGAATCCCAACGCGGATGG 1053

```


QY	1529	AAGTCAAGAGAGGGCCGCGGGCCGTCACAGGGCCGCTAGAACCGGGGTGGAGGTAG	1588
Db	1449	AAGTCAAGAGAGGGCCGCGGGCCGTCACAGGGCCGCTAGAAAGCGGGGTGGAGGTAG	1508
QY	1589	CCCTTGAGCCCTGTCCCTCGCGGCTGTAGAGACAGCAGAGACCCCTGGGCGAGTTCACAGAGAC	1648
Db	1509	CCCTTGAGCCCTGTCCCTCGCGGCTGTAGAGAGCAGCAGAGACCTCGGGCGAGTTCACAGAGAC	1568
QY	1649	CTGGGGGGTGTCTCGGGGGGTGGGGGTGGAGTGGATGTAATGTGTCTCTCTCTGGGCA	1708
Db	1569	CTGGGGGGTGTCTCGGGGGGTGGGGGTGTGACTGCTGTGAAATGTGTCTCTCTCTGGGCA	1628
QY	1709	GCTGTGGCCCTGSAATCATATGGGCGACGGAAGGGCCGCCGCCACCCCGCGCTCAACTGCTC	1768
Db	1629	GCTGTGGCCCTGTAATCATATGGGCGACGGAAGGGCCGCCGCCACCCCGCGCTCAACTGCTC	1688
QY	1769	CCGTGCAAGATTAAAGGGCTGAAATCATGAAAAAAAAAAAAAAAAAAAAA	1812
Db	1689	CCGTGCAAGATTAAAGGGCTGAAATCATGAAAAAAAAAAAAAAAAAAAAA	1732

RESULT 2
 US-08-966-316-10
 : Sequence 10 Application US/08966316
 : Patent No. 593245
 : GENERAL INFORMATION:
 : APPLICANT: Lal, Preeti
 : APPLICANT: Au-Young, Janice
 : APPLICANT: Reddy, Roopa
 : APPLICANT: Murry, Lynn E.
 : APPLICANT: Mathur, Preete
 : TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
 : NUMBER OF SEQUENCES: 18
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Incyte Pharmaceuticals, Inc.
 : STREET: 3174 Porter Drive
 : CITY: Palo Alto
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 94304
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FASTSEQ for Windows Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/966,316
 : FILING DATE: Herewith
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER:
 : FILING DATE:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Billings, Lucy J.
 : REGISTRATION NUMBER: 36,749
 : REFERENCE/DOCKET NUMBER: PF-0424 US
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 650-855-0555
 : TELEFAX: 650-845-4166
 : TELEX:
 : INFORMATION FOR SEQ ID NO: 10:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1637 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : IMMEDIATE SOURCE:
 : LIBRARY: SKINBT01
 : CLONE: 1869688
 : US-08-966-316-10
 :
 : Query Match 60.88; Score 1104.4; DB 2; Length 1637
 : Best Local Similarity 98.88; Pred. No. 1.2e-248;

us-09-762-258-1.rni

QY 1175 GACGTGAGCAGTTTGATATACCCGCTTCACACGGCAGACGCCGGTGGACAGTCTCATGAC 1234
 |||||
 Db 1254 GAGCTGAG - CAGTTTGATATACCCGCTTCACACGGCAGACGCCGGTGGACAGTCTCATGAC 1312
 |||||
 QY 1235 ACAGCCCTCAGCGGAGTGTGCACACGAGCCCTTCTGTGGCTTCATACGTAGCGCCGCTCT 1294
 |||||
 Db 1313 ACAG - CCTCAGCGGAGTGTGCACACGAGCCCTTCTGTGGGCTT - ACATTAAGTGGCGC - GTCT 1369
 |||||
 QY 1295 GTCCGTGACAG 1305
 |||||
 Db 1370 GTCTGTGACAG 1380
 |||||

RESULT 3
 US-08-749-902-4
 : Sequence 4, Application US/08749902
 : Patent No. 5985635
 : GENERAL INFORMATION:
 : APPLICANT: Bandman, Olga
 : APPLICANT: Goll, Surya K.
 : APPLICANT: Hillman, Jennifer L.
 : TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
 : TITLE OF INVENTION: PROTEIN KINASES
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 : STREET: 3174 Porter Drive
 : CITY: Palo Alto
 : STATE: CA
 : COUNTRY: US
 : ZIP: 94304

```

? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1607 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? CLONE: Consensus
US-08-749-902-4

Query Match          39.6%; Score 720; DB 2; Length 1607;
Best Local Similarity 99.1%; Pred. No. 5,5e-159;
Matches 734; Conservative 0; Mismatches 6; Indels 1; Gaps 1.

QY      874  GAGCCTGGGGGCCCTTGATGTAGACATGCTACATGAGATCGCGCCCTTATCCGACAGAA 933
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       868  GCGCGCTGGGAGCGCTGTAGTACGACATCTCTACCTGATCGCGGCCCTTTACCGAGAA 927

QY      934  CCGAGAGAAACCATGATTAAGATCATCAGGGGCAAGCTGCACACTGCCCCCTTAACCTCAC 993
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       928  CCGAGAGAAACCATGATTAAGATCATCAGGGGCAAGCTGCACACTGCCCCCTTAACCTCAC 987

QY      994  CCGAGATGCCCGGAGACCTTGTCAAAAGATTTCAGAAACGAGATCCCAAGCAGCGGATTGG 1053

```

Db 988 CCCAGATGCCCGGAGCTTGTCAAAAAGTTTCTGAAGAGGATCCAGACCGGCGATTGG 1047
QY 1054 GGGTGGCCAGGGAGTGTCTGATGTGCAGAGACATCCCTTTTCCGGACATGAATG 1113
Db 1048 GGGTGGCCAGGGAGTGTCTGATGTGCAGAGACATCCCTTTTCCGGACATGAATG 1107
QY 1114 GGACGACCTTCTGGCCCTGGCTGTGGACCCCTTTTCAGGCCCTGTCTGGAGTACAGGA 1173
Db 1108 GGACGACCTTCTGGCCCTGGCTGTGGACCCCTTTTCAGGCCCTGTCTGGAGTACAGGA 1167
QY 1174 GGACGTGAGCCAGTTTGTATCCGCTTTCACAGGCAACGCGGTGACAGTCTATGA 1233
Db 1168 GGAGGTGAGCCAGTTTGTATCCGCTTTCACAGGCAACGCGGTGACAGTCTATGA 1227
QY 1234 CACAGCCTTCAAGAGAGTGCACACAGGCTTCTGGCTTCAACATAGTGGCGCGCTC 1293
Db 1228 CACAGCCTTCAAGAGAGTGCACACAGGCTTCTGGCTTCAACATAGTGGCGCGCTC 1287
QY 1294 TGTCTGAGACGATCAAGAGAGGCTTCTCTTCACAGCCCAAGCTCGCTCAACCCAGCG 1353
Db 1288 TGTCTGAGACGATCAAGAGAGGCTTCTCTTCACAGCCCAAGCTCGCTCAACCCAGCG 1347
QY 1354 CTTCAACAGTAGCCCGCGGCTCCCGTCAAGCTTCTCCCTTTTGAAGGGTT 1413
Db 1348 CTTCAACAGTAGCCCGCGGCTCCCGTCAAGCTTCTCCCTTTTGAAGGGTT 1407
QY 1414 TCGGCCAGCCGAGCTGCGGAGCCCAAGAGTACTTACCTTCACCTCTCCAC 1473
Db 1408 TCGGCCAGCCGAGCTGCGGAGCCCAAGAGTACTTACCTTCACCTCTCCAC 1467
QY 1474 GCGCGCCCTTGACACCGCCCTTCCCATCCGTCGCCCTCCAGGAGCAGAGATG 1533
Db 1468 GCGCGCCCTTGACACCGCCCTTCCCATCCGTCGCCCTCCAGGAGCAGAGATG 1527
QY 1534 CAGAGAGGCGCGTGGCGCTTCCAGGCGCTAGAGAACCGGAGTGGGGTGAAGCCCTT 1593
Db 1528 CAGAGAGGCGCGTGGCGCTTCCAGGCGCTAGAGAACCGGAGTGGGGTGAAGCCCTT 1586
QY 1594 GAGCCCTGTCCCTGGCGCTGT 1614
Db 1587 GAGCCCTGTCCCTGGCGCTGT 1607

RESULT 4
US-09-212-771-1
; Sequence 1, Application US/09212771
; Patent No. 5958773
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
; FILE REFERENCE: RTS-0034
; CURRENT APPLICATION NUMBER: US/09/212,771
; CURRENT FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)...(1641)
US-09-212-771-1

Query Match 14.4%; Score 260.8; DB 2; Length 2610;
Best Local Similarity 56.0%; Pred. No. 8,6e-52;
Matches 562; Conservative 0; Mismatches 427; Indels 15; Gaps 3;

QY 246 ACTATGAAGGTGAGCTGACTGACACGAGTGAACGTTGGCCAGAGCGCATCGGCG 305
Db 578 ACAACTCAGGGGCTGAAGAGATGAGGTGTCTCGCCAGAGCCCAAGACACCGCTGACCA 637

QY 306 CCCACTGCTTGTAGGTGCTGCGGTGCTGGGCAAGGGGCTTAGCCAGGTGTCCAGG 365
Db 638 TGAACGAGTTTATGACTTGAAGCTGTGGGCAAGGGCACTTGTGGCAAGGTATCC --- 694
QY 366 TGGCAAGGTGCAAGGCACCACTTGGCAAAATATATGCAATGAAGTCTTAAGGAAG 425
Db 695 -----TGGTGAAGGAGAAAGCCACAGGCGCTTACCGCATGAAATCTCAAGAGG 748
QY 426 CCAAAATTTGTGCGCAATGCCAAGACACAGCACAGCAGCGGTGAGCGGAATTTTAG 485
Db 749 AAGTATGTGTGGCAAGAGCAGG---TGGCCCAACACTCACCGAAGAACCGGCTCTCG 805
QY 486 AGTACGTGAACACCCCTTATTTGTGGAATGTGGCTATGCTCTCCAGATGGTGGGAAC 545
Db 806 AAGATCCAGGACCCCTTCTCTCAACCCCTGAAGTATCTTTCAGACACAGACCGCGC 865
QY 546 TCTACCTATCTTGAATGCTCAGTGTGGGAGCTTTCACAGCATTCGAGCGAGAG 605
Db 866 TCTCTCTTGTATGAGTACGCCAAGGGGCGAGCTGTTCACACTGTCCGGGAAC 925
QY 606 GCATCTTCTGGAAGATACGCGCTGCTTCTACTGCTGAGATCAACGCTGGCCCTGGCC 665
Db 926 GTGTGTCTCCGAGGAGACCGGCGCTTCTATGCGCTGAGATGTGTACAGCCGTGACT 985
QY 666 ATCTCCACTC---CGAGGCAATCTACCGGGACCTCAAGCCCGAAGAACATCATGCTCA 722
Db 986 AACTGCACTCGGAGAAAGACGTGTGTACCGGGACCTCAAGTGGAGAACTCATGCTCG 1045
QY 723 GCAAGCAGGCGCATCAATCAATGACGACTTGTGACTGTGCAAGAGATCTTCAATGAG 782
Db 1046 ACAAGAGCGGCACTTAAGATCAGACTTGGCTGTGAAGAGAGGAGGATCAAGACG 1105
QY 783 GCGCGCTCACTCAACCTTCTGCGGCACTTGAATGATGATGACCTCTGATGTGGTG 842
Db 1106 GTGCCACATGAAGACCTTGTGGCAGACCTGAGTACTGCGCCCGAGAGTGTGAGG 1165
QY 843 GCAGTGGCCACAACGGGGGTGTGAGCTGTGAGAGCTGTGGGCGCTTATGACATGC 902
Db 1166 ACAATGACTACAGCGCTGTGATGAGAGTGTGGGCTGTGTGTATGACAGATGA 1225
QY 903 TCACTGATGCGCGCTTACCGCAGAACCCGGAAGAAACATGATGAATCATCA 962
Db 1226 TGTGGGTGCGCTGCTTACAAACAGGACATGAGAAAGCTTTTGAAGCTATCTCA 1285
QY 963 GGGCAAGCTGCACTGCGCCCTTACTCAACCCAGATGCCCGGAGCTTGTCAAAAGT 1022
Db 1286 TGGAGAGATCCGCTTCCCGGCAAGCTTGTGTCGCCAGGCAAGTCTTTCAGGGC 1345
QY 1023 TTCTGAACGGAATCCAGCAGCGGATGGGGTGGCCAGGGGATGCTGCTGATGTGC 1082
Db 1346 TGTCAAGAAAGACCCCAAGAGAGGCTTGGCGGGGCTTCCAGAGCGCAAGAGATCA 1405
QY 1083 AGAACAATCCCTTTTCCGCAATGATGAGAGCACTTGTGGCTGCGCTGTGAGAC 1142
Db 1406 TGCAGCATGCTTCTTTCGCGGTATGCTGTGGCAGCAGTACGAGAAAGCTCACCC 1465
QY 1143 CCCCTTCAAGCCCTGCTCTCACTGACAGAGAGAGTGAAGTGAAGTTCACCGCTTCA 1202
Db 1466 CACCTTCAAGGCCCAAGTACGCTCGAGACTGACACAGGTATTTGATGAGAGTTCA 1525
QY 1203 CAGGCGACAGCGCGGTGAGACAGTCTGATGACACAGCCCTCAGC 1246
Db 1526 CGGCCAGATGATCAACATCACACCACTGACCAAGATGACAGC 1569

RESULT 5
US-09-091-058-1
; Sequence 1, Application US/09091058
; Patent No. 6054285
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A.
; APPLICANT: Frech, Mathias
; TITLE OF INVENTION: Screening Method

```

1  FILE REFERENCE: 4-20683/A/20684/PCt
2  CURRENT APPLICATION NUMBER: US/09/091,058
3  CURRENT FILING DATE: 1998-06-10
4  EARLIER APPLICATION NUMBER: PCT/EP96/04814
5  EARLIER FILING DATE: 1996-11-05
6  EARLIER APPLICATION NUMBER: 9525703.6
7  EARLIER FILING DATE: 1995-12-15
8  NUMBER OF SEQ ID NOS: 23
9  SOFTWARE: Patentin Ver. 2.0
10 SEQ ID NO 1
11 LENGTH: 2610
12 TYPE: DNA
13 ORGANISM: Homo sapiens
14 FEATURE:
15 NAME/KEY: CDS
16 LOCATION: (199)..(1641)
17 OS-09-091-058-1

```

Query Match	14.4%	Score 260.8	DB 3	Length 2610
Best Local Similarity	56.0%	Pred. No. 8.6e-52		
Matches 562; Conservative	0	Mismatches 427;	Indels 15;	Gaps 3;

QY	246	ACATTGAAGAGGGTGGAGCTGACTGACACCAAGGTTGAAGCTTGCCCAAGAGGGCATCGGGC	305
Db	578	ACAACCTCAGGGGGTGAAGAAGATGTAGGGTGTCCCTGGCCAAAGCCCAAGCACCGCGTGAACA	637
QY	306	CCCACCTGCTTTGAGCTGCTGCTGCTGTGCTGGGCAAGGGGGGCTATGCGAAGGTGTTCACAG	365
Db	638	TGAACGAGTTTTGAAGTAACTGTGAAGCTCTGTGGGCAAGGGCACTTTGGGCAAGGTGAATCC---	694
QY	366	TGCGAANAAGTTGCACAAGCACCACCTTGGGCAAAATATATGCCATGAAAGTCCTAAGGAAG	425
Db	695	-----TGGTGAAGAGGAAAGGCCACAGCGCGGTACTACGCCCATGAAAGATCTCTCAAGAAAG	748
QY	426	CCAAATATGGCCGCAANTGCCAAGNACACAGCACACAGGGGCTGACGGGAACATTTAG	485
Db	749	AAGTCATCTGTGGCCAGGACGAGG---TGGCCCACTACATCAACGAGAACCGCGTCTGC	805
QY	486	AGTAGTGAAGACACCCCTTTATTTGTGGAACGTGCGCTATGCTCTCCAGACTGGTGGCAAC	545
Db	806	AGAAGCTCCAGGCAACCCCTTCTCACAAGCCTGAAAGTACTTTCCAGAACCCAGACACGCC	865
QY	546	TCCTACTCATCTTGAAGTGCCTCAGTGTGGCGAGCTCTTCAAGCATCTGAGCGAGAGG	605
Db	866	TCCTCTTTGTATGAGAGTACGCCAACGGGGGCGAGCTGTTCTTCCACATGTCGCCGGAAAC	925
QY	606	GCACTCTCTCGGAAGANTACGGGCGCTGTTTACTTGGCTGAGATACACGTGCGGCTGGGGC	665
Db	926	GTTGTTCTCTCCGAGACCGGGGCCGCTTTATGGCCCTGAGATTGTGCAAGCTCGGACT	985
QY	666	ATTCACACTC---CGAAGGCATCATCTACCGGAGCCTCAAGGCCGAGAATCATCATGCA	722
Db	986	ACCTGCACTGGAGAAAGAAAGCTGTTACCGGGACTCAAGCTGGAGAACTCATGCTGG	1045
QY	723	GCAGCCAGGGCCATCAAACTGACCGACTTTGCACTTGCAGAAGTCTATCATGAGG	782
Db	1046	ACAAGGACGGGCACATTTAATATCACAGACTTGGCGCTGTGCAAGGAGGGGATCAAGGACG	1105
QY	783	GGCGGCTACACACACCTTTGTGGGGACCATTTGATGATACATAGGCCCTTGAGATTCGTGAGC	842
Db	1106	GTTGCCACCATGAAACATCTTTTGTGGGCAACACTGATGATCTGGCCCCCGAGGTGTGGAGG	1165
QY	843	GCAGTGGCCACACACGGGGCTGTGGACTGTGGAGAGCCTGGGGGCCGATGTACGACATGC	902
Db	1166	ACATATGACTACGGCGGTGACGTGGACTGTTGGGGGCGTGGGCGTGGTCAATGACGATGA	1225
QY	903	TCACTGATCGCGCCCTTTACCGCAGAGAACCGGAAGAAAAACATGATAAGATCATCA	962
Db	1226	TGTGCGGTGCGCTCCCTTCTACACACGAGGACCATGAGAAAGCTTTTGTAGCTATCTCA	1285
QY	963	GGGGGCAAGCTGGACATCGCCCCCTACTCTACACCCCAATGCCCCGGGACCTTGTCAAAAAGT	1022
Db	1286	TGGAGGAGATCCGTTCCCGCGACGCTGTGTTCCGAGGACCAAGTCTTGTTCAGGGC	1345

QY 1023 TTTGGAAGGAATCCACGCACACGGATTGGGGGTGGCCAGAGGGATGCTGTATGTC 1082

Db 1346 TGTCTAAGAAAGAACCCCAACAGCAGGCTTGGCGGGGCTTCGAGACCGCAAGAGATCA 1405

QY 1083 AGAGACATCCCTTTTCCGGCAGCATAAATTTGGGACACCTTCTGGCCTGGCTGTGGACC 1142

Db 1406 TGCAGATCGCTTCTTTGGCGGATGCTGTGGAGCAGCTGTACGAAAGACATCAACC 1455

QY 1143 CCCCCTTAAAGCCCTGTCTGCAGTCAAGAGAGAGACTGAGCCAGTTTGATACCGCTTCA 1202

Db 1466 CACCTTTCAAGCCCAAGCTCACCTCGGAGACTACACCGAGTATTTTGTATGAGACTTCA 1525

QY 1203 CACGGCAGCGCGGTGGACAGTCCGATGACACACCTTCAGC 1246

Db 1526 CGGCCCCAGATGATCACCATCACACCACTGACCAAGATATACAGC 1569

RESULT 6
US-09-256-465-1
; Sequence 1, Application US/09256465

Query Match	Similarity	14.0%	Score 253.8	DB 3	Length 1599
Best Local	Similarity	54.0%	Pred. No. 3.2e-50		
Matches	569	Conservative	0	Mismatches 472	Indels 12
					Gaps 2
QY	313	CTTTAGAGCTGCTGCGCTGTCGTGGCGAAGGGGGGCTATGGCAAGGTCCTACAGTCGCGAAA	372		
Db	540	CTTGCAGCATCTCAAAACTCTTTGGCAAGGGAACCTTTGGCAAAAGTCATCTCGTGGGGA	599		
QY	373	GGTGCAGGCGACCAACTGEGGCAAAAATATATCCATGAATGCTTAAAGAGCCAAAT	432		
Db	600	G-----AAGGCGACACGCGCGTACTACACGCCATGAAGATCTCGGAAAAGAAATCAT	650		
QY	433	TGTGGCAATGCGCAAGGACAGACACACACGAGGGGTGAGGGGAACATTCCTAAGAGTCA	492		
Db	651	CATTGCCAAGG---ATGAAGTGCCTTCACACAGTCACCGAGCCGGGTCCTCCAGAACAC	707		
QY	493	GAAGACCCCTTATATGTTGGAAGTGGCCATGCTCTCCAGACTGATGAGCAACTGTACCT	552		
Db	708	CAGGACCCCGTTCTTCACACGTCGGCTGAAGTATGCTTTCCAGACCACGAGCCGGCTGAGCTT	767		
QY	553	CATCTTGAAGTCCCTCAGTGTGTGGGAGCTTTCACGATCTTGAAGCGAGAGGCAATCTT	612		
Db	768	TGTGATGAGTATGCCAACGAGGGGGTGAAGTGTTCCTCCACCTGTCGCGGAGACGATGCTT	827		
QY	613	CGTGAGATGAGGAGGCTGCTTCTACCTGGCTAGATCAGACGAGGGCCGCTGGGCATCTCCA	672		
Db	828	CACAGAGGAGCGGGCCCGGTTTATGTGTCAAGATGTTCTGTGGCTCTTGAGTACTTGCA	887		
QY	673	CTCCAGGAGCATCATCTACCGGAGCCTCAAGGCCGGAACATCATGCTCAGCAGCCAGGG	732		
Db	888	CTCGGGGAGCGTGTATACCGGAGACATCAAGGTGGAAAAACCTCATGCTCGAGCAAAAGATG	947		
QY	733	CCACATCAAACTGACCGGACTTGTGACTCTGCAAGAGTATATCATGAGGGCGGCTCAC	792		

Db	948	CCAAATCAAGATCTACTGACTTTTGGCCCTCTGCAAAAGAGGGCATTCAAGACGGGGCCACCAT	1007
Qy	793	TCACACCTTCGCGGCGACCAATTGATGATCAATAGGCCCCCTTGAGATTCTGTCGCGAGTGGCCA	852
Db	1008	GAAATACCTCTGTGTGGAGACCCCCGAGATGACTCTGGCCTTGAGGTGCTGGAGGACAATGACTA	1067
Qy	853	CAACGGGCGCTGTGACTGTGTGAGACCTGGGGGCGCTTGATGTACGACATGCTCATCGATC	912
Db	1068	TGGCGGGGGCGGTGACTGTAAGTGGGGGGCTGGTGTGTCATGTACGATGATGATGTGGCGCG	1127
Qy	913	GGCGGCTTTACGCGACAGAACCGGAAGAAACCATGATGATTAAGATCATCAGGGGCGACGT	972
Db	1128	CCCTGACCTTCTACAAACCAAGGACACAGACGCGCCCTCTTGAGCTCATCTCATGTGAAGAT	1187
Qy	973	GGCACTGCCCCCTTACCTCAACCCAGTCCGCGGGAGCTTGTCAAAAAGTTCTGAAACG	1032
Db	1188	CCGCTTCCCGCGGACGCTCAGCCCCGAGGCGCAAGTCCCTGCTTGGCTGGCTCTTAAGAA	1247
Qy	1033	GAATCCAGCCAGCGGATTTGGGGGTGGCCAGGGAGTGCCTGTGATGTGCAGAGCATCC	1092
Db	1248	GGACCCCAAGAGAGGCTTGGTGGGGGGCCACGATGTCGAAGAGGTGATGAGACACAG	1307
Qy	1093	CTTTTTCGCGACATGAAATTGGGACACCTTCTGGCGCTGGCTGTGTGACCCCTTTTAA	1152
Db	1308	GTTCCTTCTCAGCTCAACACGTGGAGAGACGTGGTCCAGAAAGCTCTCCACACCTTAA	1367
Qy	1153	GGCCGTGCTGCAGTACAGAGAGGAGACGCTGAGCCAGTTTGATACCCGCTTCACACGGCAC	1212
Db	1368	ACGTACAGTACAGTCCGAGGTGCACAAAGATCTTGATGATGAAATTACGGCCCATC	1427
Qy	1213	GGCGGTGACAGTCTGTGATATACACAGCCCTCAGCGAGAGTGCACCAACAGGCTTCTGG	1272
Db	1428	CATCACAATCAACACCCCTCAGCGCTATGACACGCTTGTGAGCTTGAGACCAACG	1487
Qy	1273	CTTCACATACGTGGCGCGCTGTCTCTCGGACACATCAAGAGGGGCTTCTCTTCAGCC	1332
Db	1488	GACCACTTCCCCCAAGTCTCTTACTCTGCGGACAGCTCGCGAGTAGACAGTGTGCCACG	1547
Qy	1333	CAAGCTGCGCTCACCCAGCGGCGCTCAACAGTAG	1365
Db	1548	CAGAGACGACAGCTCGCTCCATCACACGCTGG	1580
RESULT 7			
US-09-167-322-3			
Sequence 3, Application US/09167322			
Patent No. 6365151			
GENERAL INFORMATION:			
APPLICANT: Allegheny University of the Health			
Sciences, Halpern, Michael S.			
England, James M.			
TITLE OF INVENTION: CANCER VACCINE			
NUMBER OF SEQUENCES: 14			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Seidel, Gonda, Layorgna & Monaco, P. C.			
STREET: Suite 1800, Two Penn Center Plaza			
City: Philadelphia			
STATE: PA			
COUNTRY: USA			
ZIP: 19102			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patentin Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/167.322			
FILING DATE: 07-Oct-1998			
CLASSIFICATION: <Unknown>			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: PCT/US97/00582			
FILING DATE: <Unknown>			
ATTORNEY/AGENT INFORMATION:			

Query Match	14.0%	Score 253.8	DB 4	Length 1599
Best Local Similarity	54.0%	Pred. No. 3.2e-50		
Matches 569	Conservative 0	Mismatches 472	Indels 12	Gaps 2
NAME: Monaco, Daniel A. REGISTRATION NUMBER: 30.480 REFERENCE/DOCKET NUMBER: 7933-33 PC TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-8383 TELEFAX: (215) 568-5549 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1599 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-09-167-322-3				
Query	313	CTTTGAGCTGCGCTGCTGCTGGGCAAGGGGGCTATGGCTCAAGTGTCCAGTGGGAAA	372	
Db	540	CTTGACATATCTCAACACCTCTGGCAAGGAACTTTGGCAAAAGTCATCTGTGGGGA	599	
QY	373	GGTGCAGGACCAACTTGGGCAAAATATATGCCATGAAATGCTTAAGAGAGCCAAAT	432	
Db	600	G-----AAGGCACATGGCCGCTACTACCCATGAAATCTTCGCAAAAGAGTCAAT	650	
QY	433	TGTGGCGAATGCCAAGGACACAGCACACAGGGGCTGGGGCAATCTTAGATGACAT	492	
Db	651	CATTGCCAAGG---ATGAAATGCTCTACACATCACCGAAGCCGGGTCTTCAGAACAC	707	
QY	493	GAAGCACCCTTTATATGTTGGAACCTGGCCATATGCTTCGAGACTGGTGGCAACTTACCT	552	
Db	708	CAGGACCCGTTCTCTACATGGCGCTGAAGATGCTTCCAGACCCAGACCGCGCTGTCT	767	
QY	553	CATCTTATAGTCCCTCATAGTGGGGGAGACTCTTTCACGATCTGGAGCCAGAGGACATCTT	612	
Db	768	TGTGATGAGATATGCCAAACGGGGGTGAGCTGTTTCCACCTGTCCCGGAGCGTGTCT	827	
QY	613	CCTGAAATATAGGCGCTCTTCTACTGGCTGAGATCAAGCTGGGCCCTGGGCATCTCCA	672	
Db	828	CACAAAGAGAGGGGCGCGGTTTATGATGAGAAATGTCTGGGCTCTTGAATACTTGCA	887	
QY	673	CTCCAGGGGCATCATCTACCGGAGCTTAAGCCCGCAAACTATGCTCAGACCAAGG	732	
Db	888	CTCGGGGACGTGTATACCGGACATCAAGGTGAAACCTCATGTGGAAACAAAGATGG	947	
QY	733	CCACATCAAACTGACCGACCTTGGACTGTGCAGAGATCTATCCATGAGAGGGCGGTAC	792	
Db	948	CCACATCAAACTGACCTTGGACTGTGCAGAGATCTATCCATGAGAGGGCGGTAC	1007	
QY	793	TCACACTTGTGGGACCACTTGAATACATGGGCCCTGAGATCTTGTGGCGCATGGCCA	852	
Db	1008	GAAAACTTCTGTGGGACCCCGGATACCTGGCGCTAGAGTGTGGAGGACAAATGACTA	1067	
QY	853	CAACCGGCTGTGAGCTGTGGAGCTGGGGGCGCTGATGATGACGATGCTACATGATGC	912	
Db	1068	TGGCGGGGCGTGTGAGCTGTGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1127	
QY	913	GCCGCCCTTTACCGGAGAAACCGGAAAGAAAACATGATTAAGATCATCAGGGGACCT	972	
Db	1128	CTTGCCCTTTACCAACGAGCAACGACGCGCTTTCGAGCTCATCTCAGGAAGAT	1187	
QY	973	GGCAGTGGCCCCCTTACCTCAGCCAGATGCCGGGACCTTGTCAAAAAGTTTCTAAACG	1032	
Db	1188	CCGCTTCCCGGACAGCTCAGCCCGGAGGCCAAGTCTCTGTGTGGCGTGTCTTAATA	1247	
QY	1033	GAATCCCAAGGAGATTTGGGGGGGGCCCAAGGGGACCTGTGTATGTCAGAGACATCC	1092	
Db	1248	GGACCCCAAGGAGCTTTGGGGGGGGCCCAAGGATGCCAAGAGGTCTATGAGACAG	1307	
QY	1093	CTTTTCCGACATGAATTTGGAGACCTTCTGGCTGGCGGTGTGAGACCCCTTTTGAG	1152	

Db	819	ATCTATGAGAAATCGCTCTCTGGGAAGGTGGCCCTTCCCTTCCACTTCAGCTCGACCTTG	878
	1004	CGGACCTTGTCAAAAAGTTTCTGAAAGGAAATCCAGCCAGGATTTGGGGTGGCCCA	1063
Qy			
	879	AAGGACCTCGCTGGCGGAACCTCTCTGCAGGTAGATCTCACAAAGGCTTTGGGAACCTCAAG	938
Db			
Qy	1064	GGGATGCTGCTGATGTGTGCAGAGATACCTTTTCCGGACATGAAATTGGAGCACTT	1123
	939	AATGGGCTACAGATATCAAGAAACCAAGTGGTTTGGCCAACTGACTGATGTGCATC	998
Db			
Qy	1124	CTGGCTCTGTTGTGGACCCCTTCCTCAGCCCTGTCTGCAGTACAGAGAGACGTGAC	1183
Db	999	TACCAAGAGGAAGTGGAGAGTCCCTTCATACCAAAAGTTTAAAGGCCCTGGGGATTAAGAT	1056
Qy			
	1184	CAGTTTGA	1191
Db			
	1059	AACTTTGA	1066

1 Patent NO 5863780
2
3 GENERAL INFORMATION:
4
5 APPLICANT: Au-Young, Janice
6 APPLICANT: Guegler, Karl J.
7 APPLICANT: Hawkins, Phillip R.
8 TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
9
10 NUMBER OF SEQUENCES: 9
11
12 CORRESPONDENCE ADDRESS:
13 ADDRESSEE: Incyte Pharmaceuticals, Inc.
14 STREET: 3174 Porter Drive
15 CITY: Palo Alto
16 STATE: CA
17
18 COUNTRY: U.S.
19
20 ZIP: 94304
21
22 COMPUTER READABLE FORM:
23 MEDIUM TYPE: Diskette
24
25 COMPUTER: IBM Compatible
26 OPERATING SYSTEM: DOS
27
28 SOFTWARE: FASTSEQ Version 1.5
29
30 CURRENT APPLICATION DATA: 05/08/712,709
31
32 APPLICATION NUMBER: Filed Herewith
33
34 FILING DATE: Filed Herewith
35
36 ATTORNEY/AGENT INFORMATION:
37 NAME: Billings, Lucy J
38
39 REGISTRATION NUMBER: 36,749
40
41 PRIORITY/DOCKET NUMBER: PF-0118 US

```

? REFERENCE:
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-855-0555
? TELEFAX: 415-845-4166
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2311 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? IMMEDIATE SOURCE:
? LIBRARY:
? CLONE: Consensus
?
US-08-712-709-6

```

	Query Match	10.9%	Score 198.6;	DB Z:	Length	1.
	Best local Similarity	53.8%	Pred. No. 2.7e-37;			
	Matches 433; Conservative		Mismatches 369;	Indels 3;	Gaps	
OY	399 TATATTGCATGAAAGTCTTAGAAGGCCCAAAATGTCCGAATGCCACAGCACAC	458				
Dd	377 TCATGTGAGTCACAAAGTTTACAGAGAAGAACATCCTTAAMAAAGAAAGSAGAAACATA	436				
OY	459 ACACACGGCGTGAGCCGAGACATCTCTAGAGTCAGGTGAGCACCCCCTTTATGTGCAACTG	518				

Db	437	TTATGTCGAGCGGAATGTTCTGTTAAANAATGTGAACACCCCTTTCGATGAGGCGCTTC	496
OY	519	CTATGACCTTCAGACTGAGTGGGAAACTGTACCTCATCTTGAGTGCCTCAGTGGGGG	578
Db	497	ACTTCTCTTCCAGACTGCTACAAATTTGACTTTGTCTAGACTACATTAATTAAGTGGAG	556
OY	579	AGCTCTTCAACGACTGTGGAGGAGAGGGGCACTTCTCTGGAAGATACGAGCTGCTTAC	638
Db	557	AGTTGTTCTACACTCTCCAGAGGGAGACGCTGTTCTCTGGAACACAGGGGCTGTTCTATG	616
OY	639	TGCGTGAATAGCCAGTGGCGCCCGCCCATCTCCACTCCAGGGCAATCTTACCGGGAGC	698
Db	617	CTGCTGAATAATGCCAGTGGCTTGGGCTACGTACGATCAACATCGTTATAGAACT	676
OY	699	TCACGCCGAGAACATCATCTCTACAGCACCGGGGCACTCAATGACGACGACTTTGGAC	758
Db	677	TAAACACGAGAAATATTTTCTAGATTCCACAGGACACATATGCTTACGTACTTGGAC	736
OY	759	TCTGCAAGAGTCTATCATGAGGGCGCCCTCACTCACACCTTCTCGGACACTTGAAT	818
Db	737	TCTGCAAGAGACATTTGAACACACAGACACAACTCCACTTGTGTGGACGGCGAGT	796
OY	819	ACATGCGCCCTGAGATTTCGTGGCGCAGTGGGCACAAACCGGGCTGTGGACTGGTGGAGCC	878
Db	797	ATCTCCACACTAGGTGGTCTTATAGCAGGCTTATAGACAGCACTGTGGACTGGTGGTCC	856
OY	879	TGGGGGGCCGATGTACGACATGCTCACTGGATGCGCGCCCTTTACGCGAGAAACCGGA	938
Db	857	TGGAGGCTGCTGTATGTAGATGCTGATGATGGCTCGCCGCTTTTATAGCGGAACAG	916
OY	939	AGAAACCATGATATAGATCATCAGGGGCAAGCTGGCACTGCCGCCCTACACTCACCCAG	998
Db	917	CTGAATATGACGACATCTTGACACAGGCTCTCCAGCTGGAACCAATATTTCAAAATT	976
OY	999	ATGCCCGGGAACCTTGTCAAAAAGTTCTTGGAACGAGATCCACAGCGGATTTGGGGTG	1058
Db	977	CGGCAAGACACTCTCTGGAGGCTCTCTGACAAAGGACAGAAAGACGGCTCGGG--G	1033
OY	1059	GCCAGGGGATGCTGTGATGTACAGACATCCCTTTTTCGCGCACTGAAATTTGGAGC	1118
Db	1034	CCAAAGATACCTCATGAGAGATTAAGATGATGTGTTCTTCTTAAATTACTGGGATG	1093
OY	1119	ACCTTCTGGCCTGGCGTGTGGACCCCTTTTAGGCCCTGTCTGCACTCAGAGAGAGAGC	1178
Db	1094	ATCTCATTAATAAGAAATTACTCCCGCTTTTAAACCAATATGATAGTGGGCCCAAGAC	1153
OY	1179	TGAGCGAGTTGATACCGGCTTAC	1203
Db	1154	TACGCACTTGTACCCCGAGTTTAC	1178

RESULT 11
 US-09-111-444-6
 Sequence 6, Application US/09111444
 Patent No. 6045792
 GENERAL INFORMATION:
 APPLICANT: Au-Young, Janice
 APPLICANT: Guegler, Karl J.
 APPLICANT: Hakkins, Phillip R.
 TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5

us-09-762-258-1.rn

QY 1059 GCCCAGGGGATGCTGTGATTGCGACAGCAATCCCTTTTTCGGGCACATGAAITGGGACG 1118
| | | | | | | | | | | | | | | | | | | | |
Db 1034 CCAAGTAGACTTCATGAGGAGATTAAAGCATCTCTTCTTCCTTAATTAACTGGGATG 1093
QY 1119 ACCTTCGGCCTTGCGATGGGACCCTTCAGGCCCTGTCTGAGTCAGAGGAGGACG 1178
| | | | | | | | | | | | | | | | | | | | |
Db 1094 ATCTCATTAATAAAGAAGATTACTCCCCCTTTTAACCCAATGTGA GTGGGCCCAAGCAC 1153
QY 1179 TGAGCCAGTTTGATACCCCGCTTCAC 1203
| | | | | | | | | | | | | | | | | | | | |
Db 1154 TAGCGCACTTTGACCCCGAGTTTAC 1178

RESULT 12
US-09-541-228-6
; Sequence 6, Application US/09541228
; Patent No. 6232077
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

```

? COUNTRY: U.S.
? ZIP: 94304
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq Version 1.5
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/541,228
?
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/712,709
?
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Billings, Lucy J
? REGISTRATION NUMBER: 36,749
? REFERENCE/DOCKET NUMBER: PF-018 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-855-0555
? TELEFAX: 415-845-4166
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2311 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? IMMEDIATE SOURCE:
? LIBRARY:
? CLONE: Consensus
?
? US-09-541-228-6
?
? Query Match 10.9%; Score 198.6; DB 4; Length 2311;
? Best Local Similarity 53.8%; Pred. No. 2,7e-37;
? Matches 433; Conservative 0; Mismatches 369; Indels 3; Gaps
?
? QY TATATGCCATGAAAGTCCTAAGAGAGCCAAATTGTGCGCAATGCCAAGACACAGCAC 458
? | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
? Db TCTATGAGAGCAAAAGTTTACAGAAAGAAAGCAATCCTGAAAAAGAAAGAGAGATA 436
?
? QY ACAACAGCGGTGAGCGCAACATCTAGAGTCAGTGAAGCACCCCTTTATGTGCACTGG 518
? | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
? Db TTATGTGGAGCGGAAATGTTCTGTGTAAAGATGTGAAGACCCCTTCTCGTGGGCCCTTC 496
?
? QY 519 CCTATGCCCTTCACAGCTGCTGGCAAACTTACCCTATCCTCTTGAAGTGCTCAGTG 578

```

```

Db 497 ACTTCTCTTCCAGACGCTGACAAATTGACTTGTCTAGACTACATTAATAGTGGAG 556
QY 579 AGCTCTTCAGCATCTGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 638
Db 557 AGTTGTTCTACACATCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 616
QY 639 TGGTGTAGATCAGCGCTGGCCCTGGCCCTGCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 698
Db 617 CTGCTGAATAGGACAGTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 676
QY 699 TCAAGCCGAGACATGATCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 758
Db 677 TAAACAGAGAAATTTTCTCTGATTCACAGGAGACATCTTCTGCTTCTGCTTCTGCTTCT 736
QY 759 TCTGCAAGAGTATTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 818
Db 737 TCTGCAAGGAGAAATTTTCTCTGATTCACAGGAGACATCTTCTGCTTCTGCTTCTGCTTCT 796
QY 819 ACATGGCCCTGATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 878
Db 797 ATCTCCGACCTGAGTCTTCAATAGCAGCCTTATGACAGACTGTGAGCTGTGCTGTGCTGCT 856
QY 879 TGGGGCCCTGATGTAGCATGCTCATCTGATGATGATGATGATGATGATGATGATGATGAT 938
Db 857 TGGGAGCTGTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 916
QY 939 AGAAACCATGATTAAGATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 998
Db 917 CTGAATGTAGACAAACATTTCTGAACAGCCCTCAGCTGAGAACAAATTTCAAAATTT 976
QY 999 ATGCCCGGAGCTTGTCAAAAAGTTTCTGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1058
Db 977 CCGCAAGACACTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1033
QY 1059 GCCCAGGAGATCTCTGATGTGAGAGACATCCCTTTTCCGAGCATGATGAGGAGGAG 1118
Db 1034 CCAAGAGTACTTCAATGAGATTAAGATCATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1093
QY 1119 ACCTTCTGAGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1178
Db 1094 ATCTCATTAATTAAGAAATTTACTCCCTTTTAAACCAAAATGATGAGGAGGAGGAGGAG 1153
QY 1179 TGAGCCAGTTGATACCGGCTTAC 1203
Db 1154 TACGGCACTTGTACCCGAGTTTAC 1178

```

RESULT 13
US-09-031-295-1

```

: Sequence 1, Application US/09031295
: Patent No. 6326181
: GENERAL INFORMATION:
: APPLICANT: LANG, Florian
: APPLICANT: WALDEGER, Tubingen
: TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: STREET: 3000 K Street, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20007-5109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/031,295
: FILING DATE: 26-FEB-1998
: CLASSIFICATION: 435

```

```

: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 197-08-173.8
: FILING DATE: 28-FEB-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Sandcock, Colin G.
: REGISTRATION NUMBER: 31,298
: REFERENCE/DOCKET NUMBER: 058315/0123
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 672-5300
: TELEFAX: (202) 672-5399
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2370 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 43..1335
: US-09-031-295-1

```

Query Match 10.8%; Score 197; DB 4; Length 2370;
Best Local Similarity 53.7%; Pred. No. 6 4e-37;
Matches 432; Conservative 0; Mismatches 370; Indels 3; Gaps 1;

```

QY 399 TATATGCAATGAATGCTTAAAGAGGCAAAATTTGTGGCAATGCAAGACAGAC 458
Db 410 TCTATGCAATGAATGCTTAAAGAGGCAAAATTTGTGGCAATGCAAGACAGAC 469
QY 459 ACACAGGAGGCTGAGGAGCAATTTCTAGATGATGATGATGATGATGATGATGATGATGAT 518
Db 470 TTAATGTGAGGAGGAGCAATTTCTGTTGTAAGATGTAAGACCTTTCTGTGGCTTCT 529
QY 519 CCTATGCTTCCAGACTGTGCAAACTCTTACCTCATCTTGTAGTGGCTTGTAGTGG 578
Db 530 ACTTCTCTTCCAGACTGTGCAAACTCTTACCTCATCTTGTAGTGGCTTGTAGTGG 589
QY 579 AGCTCTTCAAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 638
Db 590 AGTTGTTTACCATCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 649
QY 639 TGGCTGAGATCAAGCTGTGGCCCTGGCCCTGCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 698
Db 650 CTGCTGAATTAAGCCAGTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 709
QY 699 TCAAGCCGAGAAATCAATGCTCAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 758
Db 710 TAAACACAGAGAAATTTTCTGATTTCAAGTTCAAGGAGCAATTTGCTTACTGATTTGAG 769
QY 759 TCTGCAAGAGTCTATCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 818
Db 770 TCTGCAAGAGAAATTTTCTGATTTCAAGTTCAAGGAGCAATTTGCTTACTGATTTGAG 829
QY 819 ACATGAGGCTTGAATTTGTGCTGCAAGTGGCCCAACCGGCTGTGAGTGGTGGAGCC 878
Db 830 ATCTGCACTGAGAGTGTCTTCAAGCAAGCTTATGACAGAGAGTGTGAGTGGTGGAGCC 889
QY 879 TGGGGCCCTGATGAGACATGCTCAGTCACTGATGATGATGATGATGATGATGATGATGATGAT 938
Db 890 TGGGAGCTGTCTTATGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 949
QY 939 AGAAACCATGATTAAGATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 998
Db 950 CTGAATGTAGAGAAATTTCTGAACAGCCTTCCAGCTGAGAAACCAATTTTCAAAATTT 1009
QY 999 ATGCCCGGAGCTTGTCAAAAAGTTTCTGAACAGGAGATCCACGAGGAGGATTTGGGAGT 1058
Db 1010 CCGCAAGACACTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1066
QY 1059 GCCCAGGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1118
Db 1067 CCAAGAGTACTTCAATGAGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1126

```

us-09-762-258-1.rni

OY	309	ACTGCTTTGAGCGTCGTGCCTGTGCTGGGCAAGGGGGGCTATGTGCACAGTGTTCAGGTGC	368
Db	1110	ACCGATTTTAACTTCTGTGTGTCTGGGGAAGGACGCTTTGGCAAAGT-----CATGCTC	1165
OY	369	GAAAGTGCAAGGACCACAACCTTGGGCAAAATATATGCCATTAAGAAGTCTTAAGGAAGGCCA	428
Db	1166	TCAAGAGCGGAAGGTATCA-----GATGAACTTATGCGGTGAAGATCTTAAGAAAAGATG	1220
OY	429	AAATTGTGGCCATATGCCAAGACACACACACACACACACGCGGTGAGCGGACATTTCTAGAT	488
Db	1221	TGTGTATTCAAAGATGACGATGTGGAGTGACAAATGTTGGAGAAGAGGCTGCCTGCCTGC	1280
OY	489	CAGTGAAGCACCCCTTTATTTGTGCACTGGCGCTTATGCTTCTCAACATGTGGGCAACCTC	548
Db	1281	CTGGGAAGCCCCCATTTCTCTGACTGACCTCCATTCCTCTGTTTCAACATGACACCGCCTCT	1340
OY	549	AACCTATCCTTAGAGTCTCAGTGGTGGCGAGCTCTTTCACGATCTGGAGCGAGAAGGCA	608
Db	1341	ACTTTGTATGTAGATATGTGAAGCGGGGCGACCTCATATACACATCCACMAAGTTGGCC	1400
OY	609	TCTTCTTGAAAGATACGGCCTGCTTCTAACCTGGCTGACGATACAGCTGGCCCTGGGGCCATC	668
Db	1401	GTTTCAAGAGAGCCCACATCGTATTTTACGGCTGCAGAAATTTGCCATTCGCTTTTTCTCTCT	1460
OY	669	TCCACTCCGAGGCGATCATCTACCGGAGACTCMAAGCCCGAGAACATCATGCTCAGCAAGC	728
Db	1461	TGCAGAGCAAGGGCATCATTTACCGTGACCTGAACCTTGACMACCTGATGCTGGATTTCCG	1520
OY	729	AGGGCCACATCAAACTGACCCGACTTTGGACCTCGAAGGAGTCTTTCATGAGGGCGCCG	788
Db	1521	AGGGGGCACATCAAAATATGCTGACTTTGGCATGTCTTAAGAAAGAAATCTGTGGATGGGGTGA	1580
OY	789	TCACATCACACTCTGTCGGCACCATTTGAGTACATAGGCCCTTGAGATTTCTGTGGCCAGTG	848
Db	1581	CAACCAAGACATTTCTGGACATCCAGACTACATTTGCCCAAGATCATTTGGTTATCAGC	1644
OY	849	GCCACACACCGGGTGTGATAGTGTGAGAGCTGGGGGCCCTGATATGACATGCTCATCTAGT	908
Db	1641	CCATACGAAAGTCTGTGAGATGTGTGGCGCTTTGGAATCCTGCTGTATGAATAATTGGTGCTG	1700
OY	909	GATCGCGCGCTTTACCGCGAGAGAACCGGAAGAAAAACATGATTAAGATCATCAGGGCA	968

OY	343	GGCGTATGCGAAGTGCTTCAGGTGGGAAAGTGCACGACCAACTTGGGCAAAATATA	402
Db	1123	GGGCAAGGCGACCTTCGGCAAGTGCTGCTTGCAGAGCTGGAAGGCGACAGAGAGACTAC	1182
OY	403	TGCATGAAGTCCCTAAGGAAGGCCAAAAATTGGCGCATGCCAAGACACACACACAC	462

```
Db 1183 TGGCATGAGGCGCTCGAAGAGATGTGTCTGATCGACGACGCTGGAGTGCACCAT 1242
OY 463 ACGGGCTGAGCGGAACATTTAGAGTCAGTGAACACCCCTTATTTGTGAACCTGGCTTA 522
Db 1243 GGTGAGAAAGGGGTGTGTGACTGTCCGACAGAAATCCCTTCTCACCCACCTCATCTG 1302
OY 523 TGCCTTCCAGACTGTGGCAACTCTACATCTTGAAGTCCATGAGTGTGGAGCT 582
Db 1303 CACCTTCCAGACCAGAACCCCTGTTCTTGTGATGAGTTCTCAAGGGGGGAGCT 1362
OY 583 CTTACAGCATCTGAGCGAGAGGAGCATCTCCGGAAGATACGGCTCTTACCTGGC 642
Db 1363 GATGTACCAATCCAGAGACAAAGCCGCTTGAATCTACCGTGCACGTTTATGCCGC 1422
OY 643 TGAATCAGCGTGGCCCTGGCCATCTCCACTCCAGGACATCATCTAACGGACCTCAA 702
Db 1423 TGAGATTAATGTGTGACTCAGTTTCTACAGCAAGGACATTTACAGGACCTCAA 1482
OY 703 GCCGAGAACATCATGCTCAGACGACGACCAATCAAACTGACGACTTGTGACTGTG 762
Db 1483 ACTGGACAATGTGTGTGTGACGGATGGCCACATCAAGATGGCCACTTGGGATGTG 1542
OY 763 CAAGAGTCTATCATGAGGCGCCGCTCACTACACATTTGCGGACCATTTGAGTACAT 822
Db 1543 CAAAGAGAACATATTGCGGGAGAGCGGGGCCAGACCTTTGCGGACCCCTGACTATAT 1602
OY 823 GGGCCCTGAGATTGTGTGCGGCAATGCGCACACCGGGCTGTGAGTGTGAGACTGTGG 882
Db 1603 CGCCCTGAGATCTACAGGGGCTGAGTACATTTCTGTGAGCTGTGTCTTTCGG 1662
OY 883 GGCCCTGATGTACGACATGCTCACTGATTCGCGGCCCTTTACCCAGAGAAACCGAAGAA 942
Db 1663 GGTCTTGTGTGAGATGCTCATTTGGCCATCCCGCTTCCATGTGTGATGAGATGA 1722
OY 943 AACCATGATTAAGATCATGAGGGCAAGCTGGCACTGCCCCCTAACCCTACCCAGATGC 1002
Db 1723 ACTCTTCAGTCCATCCCTGTGGACAGCCACATTTATCCCGCTGATCAACAAAGAGTC 1782
OY 1003 CCGGACCTTGTCAAAAAGTTTGAAGAACGAATCCCAAGCGGATTTGGGGGTGGCC 1062
Db 1783 CAAGGACATCTCTGAGAAAGCTCTTGAAGGGAACCAACCAAGAG-----CT 1830
OY 1063 AGGGATGCTGCTGATGTCAGAGACATCCCTTTTCCGGACATGATTTGGAGCAGCT 1122
Db 1831 GGGATGACGGGAAACATCAAAATCCACCCCTTCTCAAGACATTAATGACTCTGCT 1890
OY 1123 TCTGGCTGGGCTGTGAGACCCCTTTACGGCCCTGTGTGAGTCAAGAGAGAGCTGAG 1182
Db 1891 GGAAGACGGAGGTGTGAGCCACCCCTTACGGCCCAAGTGAAGTCAACCCAGAGACTACAG 1950
OY 1183 CCACTTGTATACCGCTTCAACGCGAGCGCGGTGAGACATGCTGATGACAGCCCT 1242
Db 1951 TAACTTTGACCAGAGATTCTGTAACGAGAAAGGCGCCTCTCTACAGCGACAAAGAACT 2010
OY 1243 CAGGAGAGTGCACACAG---GCTTCTGGGCTTACATAGTGTGGCGCTGTCTCT 1299
Db 2011 CATCGACTCCATGACCATGCTGATTCGCTGCTTCTCTGTAACCCCAATTCGA 2070
OY 1300 GGACAGCATCAAGAGGGCTTCTCT 1325
Db 2071 GCACCTCTGAGAGATTGAGTTCT 2096
```

Search completed: November 18, 2002, 00:30:07
Job time : 93 secs

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2002, 19:24:03 ; Search time 3313 Seconds

(without alignments)
15952.519 Million cell updates/sec

Title: US-09-762-258-1

Sequence: 1 gagagagagagagagaga.....aaaaaaaaaaaaaaaa 1816

Scoring table: IDENTITY_NUC

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

```
Minimum DB seq length: 0
```

Maximum DB seq length: 200000000000

Pre-processing:	Minimum Match	0%
Post-processing:	Minimum Match	0%

Listing first 45 summaries

Database :

1: genbmb.*
2: gb_hhg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pac.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_scs.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_hum.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_scs.*
28: em_un.*
29: em_vl.*
30: em_hhg_hum.*
31: em_hhg_inh.*
32: em_hhg_other.*
33: em_hhg_mus.*
34: em_hhg_pln.*
35: em_hhg_rod.*
36: em_hhg_mam.*
37: em_hhg_vrt.*
38: em_sy.*
39: em_hhg_hum.*
40: em_hhg_mus.*
41: em_hhg_other.*

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query	Length	ID	Description
1	1735	95.5	1735	9	AB016869 Homo sapi
2	1731	95.3	1807	9	BC000094 Homo sapi
3	1724	94.9	1732	6	AR206888 Sequence
4	1723	94.9	1788	9	BC006106 Homo sapi
5	1711.4	94.1	1720	9	AF099739 Homo sapi
6	1708	94.2	1716	9	AF076931 Homo sapi
7	1685.4	92.8	1744	9	AB019245 Homo sapi
8	1161.6	64.0	1491	10	MMU07938 Mus muscu
9	720	39.6	1607	6	AR086879 Sequence
10	628.8	34.6	1800	10	RAT56PK13
11	628.2	34.6	2287	10	RAT56PK
12	619.8	34.1	1778	4	OCG3PK
13	619.8	34.1	1791	9	HUMP70S6KB
14	619.8	34.1	2346	6	AX333655
15	619.8	34.1	2346	6	HUMP70S6KA
16	615.8	33.9	1717	5	XJAI31521
17	514	28.3	2399	3	DMU66562
18	514	28.3	2556	6	AE9489
19	514	28.3	2556	6	A72166
20	512.4	28.2	2481	3	DMU67304
21	500	27.5	3479	3	AY095090
22	487.8	26.9	1114	10	BC005694
23	463.2	25.5	1775	3	AF283407
24	455.6	25.1	843	6	AX250156
25	436	24.0	2770	3	AF294915
26	422.2	23.2	135116	2	AP002437
27	422.2	23.2	168567	2	AP003419
28	422.2	23.2	169144	2	AC005849
29	394.8	21.7	199814	3	CEY47D3A
30	371.6	20.5	663	5	XHP70S6
31	354.8	19.5	3131	10	RATNSK1X
32	337	18.6	2791	9	AX019387
33	337	18.6	2791	9	HSRNASR6K
34	337	18.6	3982	9	BC002363
35	337	18.6	4098	9	AK095751
36	337	18.6	5673	6	AX281711
37	334	18.4	3206	9	BC014966
38	333.8	18.4	1620	9	HUMS6K1NB
39	332.4	18.3	3061	6	AX409499
40	332.4	18.3	3061	9	HUMS6K1NA
41	331.4	18.2	3617	9	AB060213
42	331.2	18.2	413	6	AX407534
43	317.6	17.5	5240	10	MMUJ13021
44	305.8	16.8	594	6	AX282912
45	302.4	16.7	3710	5	CHKS6K1IA

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

AB016869 1735 bp mRNA linear PRI 13-NOV-1996

DEFINITION Homo sapiens mRNA for p70 ribosomal S6 kinase beta, complete cds.

VERSION AB016869.1 GI:3882084

KEYWORDS p70 ribosomal S6 kinase beta.

SOURCE Homo sapiens human embryonic kidney cell_line:HEK293 CDNA to mRNA.

ORGANISM Homo sapiens

REFERENCE 1 (sites) Gout, I., Minami, T., Hara, K., Tsujishita, Y., Filonenko, V., Waterfield, M.D. and Yonezawa, K.

AUTHORS Molecular cloning and characterization of a novel p70 S6 kinase.

TITLE

FEATURES	source
<p>Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov</p> <p>Series: IRAL Plate: 7 Row: h Column: 4</p> <p>This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 4165310.</p> <p>Location/Qualifiers</p> <p>1. 1807</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="locusid:6199"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="MGC:1848 IMAGE:3508140"</p> <p>/tissue_type="Brain, neuroblastoma"</p> <p>/clone_id="NIH_MGC_19"</p> <p>/lab_host="DH10B-R"</p> <p>/note="vector: pOTB7"</p> <p>65. 1513</p> <p>/codon_start=1</p> <p>/product="ribosomal protein S6 kinase, 70kd, polypeptide 2"</p> <p>/protein_id="AAH00094.1"</p> <p>/db_xref="GI:12652691"</p> <p>/translation="MAAVFDLDTETEGSGEGEPETSPADPCIAELRAAGLEPPVGH YEVELTSTSYNNGPERIGPCFELRLVLCGGGKGYQYKVGCTNIGKTYAKVILK KAKIVRNKADTAHTRAEKNILIESKHPIVLAFAFGKLYLILELSEGLFTH EKEGFLFEDTACFYLAETLALGHLHSGIILYROLKPEINMLSSQGHKTLDFELCKE SIHGCAVTHTPFCGLEWMAPEILVRSGHNRADVMSGALMYDMITGSPPTAENRRKK TMDIKIRKIALPPYLPDARDLVKCKFLKRNPSORIGSGPDADVORHPPFRIMND DLAMRWDPPTPLOSSEEDVSOFTDRTPTVPSDDPTALSSANOAELGTFYVA SVDSIKGSEFQPKLSRRLNSPRVPSYPSLSPFEEGRPSPLPEPELPLPLPL LPPEPSTALPLRPSPGKLSKRGKRPGR"</p>	<p>RESULT 2</p> <p>LOCUS BC000094</p> <p>DEFINITION Homo sapiens, ribosomal protein S6 kinase, 70kD, polypeptide 2, clone MGC:1848 IMAGE:3508140, mRNA, complete cds.</p> <p>ACCESSION BC000094</p> <p>VERSION BC000094.1</p> <p>KEYWORDS GI:12652690</p> <p>SOURCE MGC.</p> <p>ORGANISM Homo sapiens.</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>REFERENCE 1 (bases 1 to 1807)</p> <p>AUTHORS Strausberg, R.</p> <p>TITLE Direct Submission</p> <p>JOURNAL Submitted (03-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA</p> <p>REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov</p> <p>COMMENT Contact: MGC help desk</p> <p>Email: cgapbs-rt@mail.nih.gov</p> <p>Tissue Procurement: ATCC</p> <p>cDNA Library Preparation: Rubin Laboratory</p> <p>cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)</p> <p>DNA Sequencing by: Institute for Systems Biology</p> <p>http://www.systemsbiology.org</p> <p>contact: amadan@systemsbiology.org</p> <p>Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Kettelman and Anuradha Madan</p>

Query Match	95.3%	Score 1731:	DB 9:	Length 1807:
Best Local Similarity	100.0%:	Pred. No. 0:	Mismatches 0:	Indels 0:
Matches 1731:	Conservative	0:	Mismatches	0:
0Y	86	GGCCACACGGGGCCCCGGGGGGCCGGCGCCGCATGAGGCGCCGTGTTGATTTGGATTTGGAG	145	
Db	35	GGCCGACGGGGCCCCGGGGGGCCGGCGCCGCATAGGGCGCGGTGTTGATTTGGATTTGGAG	94	
0Y	146	ACGGAAGAAAGCAGCGAGGGGCGAGGGCGCAGAGCTCAGCCCGCGAGCATGTGCC	205	
Db	95	ACGGAGGAAGGCAGCGAGGGGCGAGGGCGAGCAGACTCAGCCCCCGGACGATGTGCC	154	
0Y	206	CTTGGCGAGTTAAGGGCACTGTGGCCCTAGAGCCGTGTGGAGCCATATGAAGAGGTGGAGCTG	265	
Db	155	CTTGGCGAGTTAAGGGCACTGTGGCCCTAGAGCCGTGTGGAGCCATATGAAGAGGTGGAGCTG	214	
0Y	266	ACTGAGACCAAGGCTAAACCTTGGCCAGAGCCATGAGGGCCCGACACTGCTTGGAGCTGTG	325	
Db	215	ACTGAGACCAAGGCTAAACCTTGGCCAGAGCCATGAGGGCCCGACACTGCTTGGAGCTGTG	274	
0Y	326	CGTGTGCTGGGCAAGGGGGGCTATGGCAAGTGTTCACAGGTGCGAAAGGTGCAAGCCACC	385	
Db	275	CGTGTGCTGGGCAAGGGGGGCTATGGCAAGTGTTCACAGGTGCGAAAGGTGCAAGCCACC	334	
0Y	386	AACCTTGGCGAAAAATATATCCATGAAAGTCCTAAGGAAGGCCAAAATTTGGCGCAATGGCC	445	
Db	335	AACCTTGGCGAAAAATATATCCATGAAAGTCCTAAGGAAGGCCAAAATTTGGCGCAATGGCC	394	
0Y	446	AAGGACACAGCACACACAGCGGGCTGAGCGGAACTTCTAGTACAGTGAAGCACCCCTTT	505	
Db	395	AAGGACACAGCACACACAGCGGGCTGAGCGGAACTTCTAGTACAGTGAAGCACCCCTTT	454	
0Y	506	ATTGTGGAACGTGGCCTATATCCCTTCCAGACTGGTGGCAAACTTACTCATCTTGTAGTGC	565	
Db	455	ATTGTGGAACGTGGCCTATATCCCTTCCAGACTGGTGGCAAACTTACTCATCTTGTAGTGC	514	
0Y	566	CTCAGTGGTGGGGAGGTCTTTCACGCCTCTGGAGACGAGAGGGCCATCTTCGGAAGATACG	625	
Db	515	CTCAGTGGTGGGGAGGTCTTTCACGCCTCTGGAGACGAGAGGGCCATCTTCGGAAGATACG	574	
0Y	626	GCCTGCTTACCTGGCTAGATCACGCTGTGGCCCTGGGCCATCTCCACTGCCAGGGCATC	685	
Db	575	GCCTGCTTACCTGGCTAGATCACGCTGTGGCCCTGGGCCATCTCCACTGCCAGGGCATC	634	
0Y	686	ATCTACCGGGACTCAAGCCCGAGAACATATATCTTAGACAGCCAGGGCCACATCAAACTG	745	
Db	635	ATCTACCGGGACTCAAGCCCGAGAACATATATCTTAGACAGCCAGGGCCACATCAAACTG	694	
0Y	746	ACCGACTTTGGACTCTGCAGAGAGTATTATCAGAGAGGGGCGCTCACTCACTCTTGTGC	805	
Db	695	ACCGACTTTGGACTCTGCAGAGAGTATTATCAGAGAGGGGCGCTCACTCACTCTTGTGC	754	
0Y	806	GGCACCATTTAGATACATGGCCCTCGAGATTCTGGTGCAGAGTGCCACAACCGGGCTGTG	865	
Db	755	GGCACCATTTAGATACATGGCCCTCGAGATTCTGGTGCAGAGTGCCACAACCGGGCTGTG	814	
0Y	866	GACTGTGGAAGCCTGGGGGGCCTGATGTACAGATCTCACTGGATTCGCCGCCCTTTACC	925	
Db	815	GACTGTGGAAGCCTGGGGGGCCTGATGTACAGATCTCACTGGATTCGCCGCCCTTTACC	874	
0Y	926	GGAGAGAACCCGGAAGAAACCATGATTAAGATATCATAGGGGCAAGGTGGCATGTGCCCCC	985	
Db	875	GGAGAGAACCCGGAAGAAACCATGATTAAGATATCATAGGGGCAAGGTGGCATGTGCCCCC	934	
0Y	986	TACCTTACCCAGATGCCCGGGACCTTGTCTAAAAAGTTTCTGAACGGAAATCCAGCCAG	1045	
Db	935	TACCTTACCCAGATGCCCGGGACCTTGTCTAAAAAGTTTCTGAACGGAAATCCAGCCAG	994	
0Y	1046	CGGATTTGGGGGTGGCCAGGGGATGCTGCTGATGTGTCAAGACATCCCTTTTTCGGGCAC	1105	
Db	995	CGGATTTGGGGGTGGCCAGGGGATGCTGCTGATGTGTCAAGACATCCCTTTTTCGGGCAC	1054	

QY	1106	ATGAATTTGGGACACCTTTGGCCCTGGGCGTGGAGACCCCTTTACAGGCGCTGTGGAG	1165
Db	1055	ATGAATTTGGGACACACCTTTGGCCCTGGGCGTGGAGACCCCTTTACAGGCGCTGTGGAG	1114
QY	1166	TCAGAGGAGGACGTGAAGCCATTGTATACCCCTTCACAGGCGAGACGCGGTGACAGT	1225
Db	1115	TCAGAGGAGGACGTGAAGCCATTGTATACCCCTTCACAGGCGAGACGCGGTGACAGT	1174
QY	1226	CCTGATGACACAGCCCTCAGGCGAGAGTGGCAACACAGGCTTCTGTGGCTTTCACATACGTG	1285
Db	1175	CCGTGATGACACAGCCCTCAGGCGAGAGTGGCAACACAGGCTTCTGTGGCTTTCACATACGTG	1234
QY	1286	GGCGCGTCTGTCTGGACAGCATCAAGAGGGGCTTCTCTTCAGGCGCAAGCTGGCGCTGA	1345
Db	1235	GGCGCGTCTGTCTGGACAGCATCAAGAGGGGCTTCTCTTCAGGCGCAAGCTGGCGCTGA	1294
QY	1346	CCGAGGCGCCTCAACAGTAGCCGCCGGGATCCCGTCAGGCGCCCTCAAGTTCCTCCCTTTT	1405
Db	1295	CCGAGGCGCCTCAACAGTAGCCGCCGGGATCCCGTCAGGCGCCCTCAAGTTCCTCCCTTTT	1354
QY	1406	GAGGGGTTTCGGGCCACAGCCCTGCGGAGGCCACGAGCTACCTCTACCTCCATC	1465
Db	1355	GAGGGGTTTCGGGCCACAGCCCTGCGGAGGCCACGAGCTACCTCTACCTCCATC	1414
QY	1466	CTGGCACCGCCGCGCCCTGACACAGCCGCCCTCTCCCATCGTCCGCCCTCAGGAGAC	1525
Db	1415	CTGGCACCGCCGCGCCCTGACACAGCCGCCCTCTCCCATCGTCCGCCCTCAGGAGAC	1474
QY	1526	AAGAATCCCAAGAGGGGCGCTGGGGCTCCAGGCGCTAGGAAGCGGGGTGGGGTAGGG	1585
Db	1475	AAGAATCCCAAGAGGGGCGCTGGGGCTCCAGGCGCTAGGAAGCGGGGTGGGGTAGGG	1534
QY	1586	TAGCCCTTAGCCCTGTCTCCCTGCTGGCTGTGAAGACACAGACACCTGGGCCAGTTCACA	1645
Db	1535	TAGCCCTTAGCCCTGTCTCCCTGCTGGCTGTGAAGACACAGACACCTGGGCCAGTTCACA	1594
QY	1646	GACCTGGGGGCTGTGCTGGGGGGTGGGGGTGTGAGTGGGTGAAGGTGTGCTGTGGGG	1705
Db	1595	GACCTGGGGGCTGTGCTGGGGGGTGGGGGTGTGAGTGGGTGAAGGTGTGCTGTGGGG	1654
QY	1706	GCAGCTGTGCCCTCAATCATGTGGGACGAGAGGGCGCCGCCACACCCCGCCTCAACTG	1765
Db	1655	GCAGCTGTGCCCTCAATCATGTGGGACGAGAGGGCGCCGCCACACCCCGCCTCAACTG	1714
QY	1766	CTCCCGCTGGAGATTAAAGGCTGAATCATGAAAAA	1816
Db	1715	CTCCCGCTGGAGATTAAAGGCTGAATCATGAAAAA	1765
RESULT 3			
AR206888			
LOCUS	AR206888	1732 bp	DNA
DEFINITION	Sequence 1 from patent US 6372467.		linear
ACCESSION	AR206888		
VERSION	AR206888.1	GI:21505626	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1732)		
AUTHORS	Blenis,J., Lee-Fruman,K.K. and Kuo,C.J.		
TITLE	P5456k and p5586k genes, proteins, primers, probes, and detection methods		
JOURNAL	Patent: US 6372467-A 1 16-APR-2002;		
FEATURES	Location/Qualifiers		
source	1..1732		
BASE COUNT	355 a 532 c 532 g	313 t	
ORIGIN	/organism="unknown"		
Query Match	94.9%:	Score 1724:	DB 6; Length 1732:
Best Local Similarity	100.0%:	Pred. NO. 0;	
Matches 1724;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;

QY	89	CGACGGCCCCCGGGGGCCGGGGCCCGCCATGGGCGCCGCTGTTGATTTGGATTTGGAGAGC	144
Db	9	CGACGGCCCCCGGGGGCCGGGGCCCGCCATGGGCGCCGCTGTTGATTTGGATTTGGAGAGC	68
QY	149	GAGGAAGCGACGAGGCGGAGGCGAGCGACAGAGCTCAGCCCCCGGCGAGCGATGCCCTT	208
Db	69	GAGGAAGCGACGAGGCGGAGGCGAGCGAGCGACAGAGCTCAGCCCCCGGCGAGCGATGCCCTT	128
QY	209	GCCGAGTTGAGGGCAGCGTGGCGCTTAGACCTGTGGGACACTATGAAAGGTGGAGCTGACT	268
Db	129	GCCGAGTTGAGGGCAGCGTGGCGCTTAGACCTGTGGGACACTATGAAAGGTGGAGCTGACT	188
QY	269	GAGACACACGCGAAAGCTTTGGGCCCGAGAGCGGATCGGGGCCCACTGCTTTGAGCTGCGGT	328
Db	189	GAGACACACGCGAAAGCTTTGGGCCCGAGAGCGGATCGGGGCCCACTGCTTTGAGCTGCGGT	248
QY	329	GTCGTGGGCAGAGGGGGCTATGCGAGGTGTTCCAGGTGCGAAAGGTGCAGGCAACAC	388
Db	249	GTCGTGGGCAGAGGGGGCTATGCGAGGTGTTCCAGGTGCGAAAGGTGCAGGCAACAC	308
QY	389	TTGGCCAAATATATATGCCATGAAGTCTTAAGGAAGGCGAAATTTGGCCAAATGGCCAA	448
Db	309	TTGGCCAAATATATATGCCATGAAGTCTTAAGGAAGGCGAAATTTGGCCAAATGGCCAA	368
QY	449	GACACAGCACACACAGGGGCTGAGCGGAACTTCTAGAGTCAGTGAAGCACCCCTTTATTT	508
Db	369	GACACAGCACACACAGGGGCTGAGCGGAACTTCTAGAGTCAGTGAAGCACCCCTTTATTT	428
QY	509	GGGGAACGTGGCCCTTATGCTTCCAGCTGGGGGCAAACTCACTCACTCTTGAGTGCCTC	568
Db	429	GTCGAACTGGCCTTATGCTTCCAGACTGGTGGCAAACTTCACTCACTCTTGAGTGCCTC	488
QY	569	AGTGTGGCGAGCTTCTCACGACATCTGAGAGCGAAGGGGCATCTTCTGGAAGATAGGGCC	628
Db	489	AGTGTGGCGAGCTTCTCACGACATCTGAGAGCGAAGGGGCATCTTCTGGAAGATAGGGCC	548
QY	629	TGCTTCTACCTGGCTGAGATACGCTTGGCCCTGGGCCATCTCCACTCCAGGGCATCATC	688
Db	549	TGCTTCTACCTGGCTGAGATACGCTTGGCCCTGGGCCATCTCCACTCCAGGGCATCATC	608
QY	689	TACCGGACCTCAAGCCCGAGACATCATGCTCAGCGAGCCAGGGCCACATCAAACTGAGC	748
Db	609	TACCGGACCTCAAGCCCGAGACATCATGCTCAGCGAGCCAGGGCCACATCAAACTGAGC	668
QY	749	GACTTTGGACTCTGCAAGAGACTATCATGAGGGCGCGCTCACTCACACCTTCTGGGC	808
Db	669	GACTTTGGACTCTGCAAGAGACTATCATGAGGGCGCGCTCACTCACACCTTCTGGGC	728
QY	809	ACCATGAGTACATGGGCCCTGAGATCTGTGGCGAGTGGCCACAAACGGGCTGGAGC	868
Db	729	ACCATGAGTACATGGGCCCTGAGATCTGTGGCGAGTGGCCACAAACGGGCTGGAGC	788
QY	869	TGCTGGACCTGGGGGGCCCTGATGTACAGATGCTCACTGATCGCGCGCCTTTACCGCA	928
Db	789	TGCTGGACCTGGGGGGCCCTGATGTACAGATGCTCACTGATCGCGCGCCTTTACCGCA	848
QY	929	GAGAACCGGAAGAAACCATGATGATCATCAGGGGCAAGCTGGCACTGCCCTCTAC	988
Db	849	GAGAACCGGAAGAAACCATGATGATGATCATCAGGGGCAAGCTGGCACTGCCCTCTAC	908
QY	989	CTCACCCCAAGATGGCCCGGAGCCTTGTCAAAAGTTTCTGAAAGGAAATCCAGCCAGCGG	1044
Db	909	CTCACCCCAAGATGGCCCGGAGCCTTGTCAAAAGTTTCTGAAAGGAAATCCAGCCAGCGG	968
QY	1049	ATTGGGGGTGGCCCAAGGGAGTGTGCTGATGTGCAGAGACATCCCTTTTCCGGCCATG	1104
Db	969	ATTGGGGGTGGCCCAAGGGAGTGTGCTGATGTGCAGAGACATCCCTTTTCCGGCCATG	1024
QY	1109	AATTGGGACACACTTTCTGGGCTTGGCGTGTGGAGACCCCTTTCAAGGCCCTGTCTGCAGTA	1164
Db	1029	AATTGGGACACACTTTCTGGGCTTGGCGTGTGGAGACCCCTTTCAAGGCCCTGTCTGCAGTA	1084


```
|||||
Db 429 ATGTGGAACTGGCCTTGGCTTCACAGCTGTGGGCAACCTTACCTTCATCTTGTAGATGC 488
QY 566 CTCAGTGTGGCAGCTCTTTCACGATCTGAGAGAGAGGACATCTTCCTGGAAGATACG 625
Db 489 CTCAGTGTGGCAGCTCTTTCACGATCTGAGAGAGAGGACATCTTCTGGGAAGATACG 548
QY 626 GCTGTCTTCACTGCTGAGATACGCTGGCCCTGGGCAATCTCACTCCAGGCAATC 685
Db 549 GCTGTCTTCACTGCTGAGATACGCTGGCCCTGGGCAATCTCACTCCAGGCAATC 608
QY 686 ATCTACCGGGACCTCAAGCCCGGAGAAATCATGTCTCAGCAGCCAGGCGCACATTAAC 745
Db 609 ATCTACCGGGACCTCAAGCCCGGAGAAATCATGTCTCAGCAGCCAGGCGCACATTAAC 668
QY 746 ACCGACTTTGGACTCTGCAAGAGAGTCTATCCATGAGGGCCCGCTCACTCAACCTTCTGC 805
Db 669 ACCGACTTTGGACTCTGCAAGAGAGTCTATCCATGAGGGCCCGCTCACTCAACCTTCTGC 728
QY 806 GGCACCATTTAGTACATGCCCCCTGAGATTCTGTGCGCAGTGGCCAAACCGGGCTGTG 865
Db 729 GGCACCATTTAGTACATGCCCCCTGAGATTCTGTGCGCAGTGGCCAAACCGGGCTGTG 788
QY 866 GACGTGTGGAGCCTGGGGGCGCTGATGTAGACATGCTCACTGGATGGCCGCTTTAC 925
Db 789 GACGTGTGGAGCCTGGGGGCGCTGATGTAGACATGCTCACTGGATGGCCGCTTTAC 848
QY 926 GCAGAGAACCGGAGAAACCATGATAGATCATCAGGGGCAAGTGGCACTGCCCC 985
Db 849 GCAGAGAACCGGAGAAACCATGATAGATCATCAGGGGCAAGTGGCACTGCCCC 908
QY 986 TACCTCACCCAGATGCGCGGACCTTGTCAAAAAGTTTCTGAAAACGGAATCCAGCCAG 1045
Db 909 TACCTCACCCAGATGCGCGGACCTTGTCAAAAAGTTTCTGAAAACGGAATCCAGCCAG 968
QY 1046 CGGATTGGGGGTGGCCCAAGGGAGTGTCTGATGTGAGAGACATCCCTTTTCCGGCAC 1105
Db 969 CGGATTGGGGGTGGCCCAAGGGAGTGTCTGATGTGAGAGACATCCCTTTTCCGGCAC 1028
QY 1106 ATGAATTTGGGACGACCTTCTGGCCCTGGCGTGTGAGACCCCTTTTCAGGGCCCTGTG 1165
Db 1029 ATGAATTTGGGACGACCTTCTGGCCCTGGCGTGTGAGACCCCTTTTCAGGGCCCTGTG 1088
QY 1166 TCAGAGAGAGACGTGAGACCATTTGATACCCGCTTCACAGCAGACGCCGGTGGACAGT 1225
Db 1089 TCAGAGAGAGACGTGAGACCATTTGATACCCGCTTCACAGCAGACGCCGGTGGACAGT 1148
QY 1226 CTTGATGACACAGCCCTCAGCAGAGAGTGGCCACAGGCGCTTCCTGGGCTTCACATACGTG 1285
Db 1149 CTTGATGACACAGCCCTCAGCAGAGAGTGGCCACAGGCGCTTCCTGGGCTTCACATACGTG 1208
QY 1286 GCGCCCTGTGTCTGAGACATCAAGAGAGGCTTCTCTTCAGGCCCAAGCTGCGCTCA 1345
Db 1209 GCGCCCTGTGTCTGAGACATCAAGAGAGGCTTCTCTTCAGGCCCAAGCTGCGCTCA 1268
QY 1346 CCCAGAGGCGCTCAACAGTACGCCCCGGGCTCCCGCTCAAGCTTCTCCCTTTT 1405
Db 1269 CCCAGAGGCGCTCAACAGTACGCCCCGGGCTCCCGCTCAAGCTTCTCCCTTTT 1328
QY 1406 GAGGGGTTTTGGGCGCAGCCCGCAGCTGCGGAGGCCACAGGAGTACCTTCACTCCACATC 1465
Db 1329 GAGGGGTTTTGGGCGCAGCCCGCAGCTGCGGAGGCCACAGGAGTACCTTCACTCCACATC 1388
QY 1466 CTGCAACCGCCGCGGCTTGCAGACCGCCGCTCTCCCAATCCGCTCCCTCAGGGAC 1525
Db 1389 CTGCAACCGCCGCGGCTTGCAGACCGCCGCTCTCCCAATCCGCTCCCTCAGGGAC 1448
QY 1526 AAGAATCCCAAGAGGGCGCTGGGCTCCAGGGCGCTAGAGAACCCGGGTGGGGTGAAGG 1585
Db 1449 AAGAATCCCAAGAGGGCGCTGGGCTCCAGGGCGCTAGAGAACCCGGGTGGGGTGAAGG 1508
QY 1586 TAGCCCTTAGCCCTGTCCCTGGGGCTGTGAGAGCAGAGAGACCTTGGGCAATTTCCAGA 1645
|||||
```

```
Db 1509 TAGCCCTTAGCCCTGTCCCTGGCGCTGTGAGAGCAGACAGACCTTGGGCCAATTCACAGA 1568
QY 1646 GACCTGGGGGTGTGTCTGGGGGTGGGGGTGTGAGTGCATGAAGTGTGTGTGCTGGG 1705
Db 1569 GACCTGGGGGTGTGTCTGGGGGTGGGGGTGTGAGTGCATGAAGTGTGTGTGCTGGG 1628
QY 1706 GCAGCTGTGCCCTGGAATCATGAGGACGAGAGGCGCCGCCACACCCGCGCTCAACTG 1765
Db 1629 GCAGCTGTGCCCTGGAATCATGAGGACGAGAGGCGCCGCCACACCCGCGCTCAACTG 1688
QY 1766 CTCCCTGGAAGATTTAAGGCTGATCATGAAAAAATTTTAAAAA 1816
Db 1689 CTCCCTGGAAGATTTAAGGCTGATCATGAAAAAATTTTAAAAA 1739

RESULT 5
AF099739
LOCUS AF099739 1720 bp mRNA linear PRI 24-NOV-2000
DEFINITION Homo sapiens S6 kinase-related kinase mRNA, complete cds.
ACCESSION AF099739
VERSION AF099739.1 GI:4454856
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 1720)
Koh, H., Jee, K., Lee, B., Kim, J., Kim, D., Yun, Y. H., Kim, J. W.,
Choi, H. S. and Chung, J.
Cloning and characterization of a nuclear S6 kinase, S6
kinase-related kinase (SRK); a novel nuclear target of Akt
Oncogene 18 (36), 5115-5119 (1999)
99422046
MEDLINE
10490846
PUBMED
REFERENCE
2 (bases 1 to 1720)
Koh, H. J., Lee, B. N., Choi, H. S. and Chung, J.
Direct Submission
Submitted (18-OCT-1998) Biological Sciences, Korea Institute of
Advanced Science and Technology, Kusong, Yuseong, Taejeon 305-701,
South Korea
FEATURES
source
location/Qualifiers
1..1720
/organism="Homo sapiens"
/db_xref="taxon:9606"
40..1488
/feature="SRK; similar to ribosomal protein S6 kinase,
p70-S6K"
/codon_start=1
/product="S6 kinase-related kinase"
/protein_id="AAd20990.1"
/db_xref="GI:4454857"
/translation="MAAVDDLDLETEEGSEGEPELSPADACPLAEPLRAAGLEPVGH
YEVELTSTVAVGPERIGPHGFEFLRYLKGKGVKYNQVORVQSTNIGKTYAMKVLK
KATYRNKQDTHAERARLIESYVHPITLAVAFQNGKLYLLELSGELFTLH
EBEGFLFEDTAFYLAETLALGHSQGITTRDLPENIMLSQGHILKLDGELCKE
SIHEGAVTHFEGTLEYMAPLELIVSHGNRAVDWLSLALWDMITLGSPPPTAEKRK
TMDKITRGLAPLYLPDADRDLYKFKLRNRSRIGGPGDAADVONHPFRHNMD
DLARVDPPEPRPCLOSEEDVYQFPTRTROPVPSPTDALSESANQAFGFTYVAP
SVLDSIKRGEFSOPKLRSPRRNSPRVPSPLKRSPEGRFSPSLDEPELPLPL
LPPEPSTAPLPIRPPSGTKSKRGRRPGR"
BASE COUNT 339 a 533 c 535 g 313 t
ORIGIN
Query Match 94.2%; Score 1711.4; DB 9; Length 1720;
Best Local Similarity 99.9%; Pred No. 0;
Matches 1712; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 84 GAGCGCAGCGGCCCGCGGGCGCGCGCCCATGCGCGCGCGCTGTTGATTGGATTGG 143
Db 8 GAGCGCGCAGCGGCCCGCGGGCGCGCGCCCATGCGCGCGCGCTGTTGATTGGATTGG 67
QY 144 AGACGAGAGAGCAGCGAGGCGGAGGCGAGGCGCAGAGCTCAGCCCCCGGAGCGCATGTC 203
|||||
```

Db 68 AGACGGAGAAAGCAGCGAGGGCGAGGGCGAGCCAGAGCTACGCCCGCGAGCAGCATGTC 127
 Oy 204 CCGTTGCCAGATTGAGGGGAGCTGGCTAGAGCCGTGGGACATATGAAAGAGTGGAGC 263
 Db 128 CCGTTGCCAGATTGAGGGGAGCTGGCTAGAGCCGTGGGACATATGAAAGAGTGGAGC 187
 Oy 264 TGACTGAGACCGAGCGTGAAGCTGGGCCAGAGCGCATGGGGCCCACTGCTTTGAGCTGC 323
 Db 188 TGACTGAGACCGAGCGTGAAGCTGGGCCAGAGCGCATGGGGCCCACTGCTTTGAGCTGC 247
 Oy 324 TGCGTGTCTGGGCAAGGGGGGCTATGGCAAGTGTCTCCAGTGGCAAGGTGCAAGGCA 383
 Db 248 TGCGTGTCTGGGCAAGGGGGGCTATGGCAAGTGTCTCCAGTGGCAAGGTGCAAGGCA 307
 Oy 384 CCAATTTGGGCAAAATATATGCGATGAAGTCTTAAGAAAGGCCCAAAATTTGGGCCAATG 443
 Db 308 CCAATTTGGGCAAAATATATGCGATGAAGTCTTAAGAAAGGCCCAAAATTTGGGCCAATG 367
 Oy 444 CCAAGGACACAGCACACACAGCGGCTGAGCGGACATTTCTAGAGTCAGTGAAGCACCCCT 503
 Db 368 CCAAGGACACAGCACACACAGCGGCTGAGCGGACATTTCTAGAGTCAGTGAAGCACCCCT 427
 Oy 504 TTATTTGGAAGTGGCTATGCTTCCAGACTGTGGCAAACTCTACCTCATCTTGAAT 563
 Db 428 TTATTTGGAAGTGGCTATGCTTCCAGACTGTGGCAAACTCTACCTCATCTTGAAT 487
 Oy 564 GCGTCAGTGGCGGAGCTCTTCAAGCATCTGGAGCGAGAGGGCATCTTCTGGAAAGATA 623
 Db 488 GCGTCAGTGGCGGAGCTCTTCAAGCATCTGGAGCGAGAGGGCATCTTCTGGAAAGATA 547
 Oy 624 GCGCTGCTTCTACCTGGCTGAGTACAGCTGGCCCTGGGCAATCTCCATCCAGAGCA 683
 Db 548 GCGCTGCTTCTACCTGGCTGAGTACAGCTGGCCCTGGGCAATCTCCATCCAGAGCA 607
 Oy 684 TCATTTACCGGGAGCTCAAGCCCGAAGAACATCATCTCAGCAGCGAGGGCCACATCAAC 743
 Db 608 TCATTTACCGGGAGCTCAAGCCCGAAGAACATCATCTCAGCAGCGAGGGCCACATCAAC 667
 Oy 744 TGACCGATTTGGAGCTTCGCAAGAGTCTATCATGAGGGGCCCTCACTGCACCTTCT 803
 Db 668 TGACCGATTTGGAGCTTCGCAAGAGTCTATCATGAGGGGCCCTCACTGCACCTTCT 727
 Oy 804 GCGGACCATTTGAGTATAGTGGCCCTGAGATCTGTGGCGAGTGGCCCAACCGGGCTG 863
 Db 728 GCGGACCATTTGAGTATAGTGGCCCTGAGATCTGTGGCGAGTGGCCCAACCGGGCTG 787
 Oy 864 TGAGCTGTGAGCCTGGGGGCGCTGATGTACGACATGCTCACTGATGCGGCCCTTTA 923
 Db 788 TGAGCTGTGAGCCTGGGGGCGCTGATGTACGACATGCTCACTGATGCGGCCCTTTA 847
 Oy 924 CCGCAGAAACCGGAAAGAAACCATGATATCATCAGGGGCAAGCTGGGACATGCCCC 983
 Db 848 CCGCAGAAACCGGAAAGAAACCATGATATCATCAGGGGCAAGCTGGGACATGCCCC 907
 Oy 984 CTTACCTACCCCAATGCCCCGGGACCTTGTCAAAAAGTTTGTGAACGGAATCCAGCC 1043
 Db 908 CTTACCTACCCCAATGCCCCGGGACCTTGTCAAAAAGTTTGTGAACGGAATCCAGCC 967
 Oy 1044 AGCGGATTTGGGGGCGCCAGGGGATGCTGTGATGTGAGAGACATCCCTTTTCCGCG 1103
 Db 968 AGCGGATTTGGGGGCGCCAGGGGATGCTGTGATGTGAGAGACATCCCTTTTCCGCG 1027
 Oy 1104 ACATTAATTTGGAGACATCTTGGGCTGGCTGTGGAGCCCCCTTTCAAGGCCCTGTGCG 1163
 Db 1028 ACATTAATTTGGAGACATCTTGGGCTGGCTGTGGAGCCCCCTTTCAAGGCCCTGTGCG 1087
 Oy 1164 AGTCAGAGGAGAGCTGAGACCGATTGATACCGGCTTCAACAGCGAGAGCGCGTGGACA 1223
 Db 1088 AGTCAGAGGAGAGCTGAGACCGATTGATACCGGCTTCAACAGCGAGAGCGCGTGGACA 1147
 Oy 1224 GTCTGTATGACACAGCCTCTCAGCGAGAGTCCCAACCGAGCCTTCTGGGCTTCAACATG 1283
 Db 1148 GTCTGTATGACACAGCCTCTCAGCGAGAGTCCCAACCGAGCCTTCTGGGCTTCAACATG 1207

Oy 1284 TGGCGCCGCTCTCTCTGGAACACATCAAGAGAGGCTTCTCTCCAGCCCAAGCTGCCCT 1343
 Db 1208 TGGCGCCGCTCTCTCTGGAACACATCAAGAGAGGCTTCTCTCCAGCCCAAGCTGCCCT 1267
 Oy 1344 CACCCAGGCGCTTCAACAGTAGACCCCGGGTCCCGCTCAGCCCTCAAGTTCTCCCTT 1403
 Db 1268 CACCCAGGCGCTTCAACAGTAGACCCCGGGTCCCGCTCAGCCCTCAAGTTCTCCCTT 1327
 Oy 1404 TTGAGGGGTTTGGGCGCAGCCCGGCTGCGGAGCCCGGAGGCTACTCTACTCTCCAC 1463
 Db 1328 TTGAGGGGTTTGGGCGCAGCCCGGCTGCGGAGCCCGGAGGCTACTCTACTCTCCAC 1387
 Oy 1464 TCCCTGCAACCGCGCGCGCTGAGCAGCGCCCTCTCCCTCCATCCGTCGCCCTCAGGA 1523
 Db 1388 TCCCTGCAACCGCGCGCGCTGAGCAGCGCCCTCTCCCTCCATCCGTCGCCCTCAGGA 1447
 Oy 1524 CCAAGAGTCCAAAGAGGGGCGTGGGCGTCCAGGGCGCTAGGAAGCCGGGTGGGGTGAG 1583
 Db 1448 CCAAGAGTCCAAAGAGGGGCGTGGGCGTCCAGGGCGCTAGGAAGCCGGGTGGGGTGAG 1507
 Oy 1584 GGTAGCCCTTGAGCCTCTGTCCCTGCGGCTGTGAGAGCAGACAGACCTTGGCCACTTCA 1643
 Db 1508 GGTAGCCCTTGAGCCTCTGTCCCTGCGGCTGTGAGAGCAGACAGACCTTGGCCACTTCA 1567
 Oy 1644 GAGACCTGGGGGTGTGTCTGGGGGTGGGGGTGTGAGTGTGTAAGAGTGTGTCTGCTG 1703
 Db 1568 GAGACCTGGGGGTGTGTCTGGGGGTGGGGGTGTGAGTGTGTAAGAGTGTGTCTGCTG 1627
 Oy 1704 GGGCAGCTGTGCCCCCTGATATCGGGGCAAGAGGGCGCGCCCAACACCCCGCTCAAC 1763
 Db 1628 GGGCAGCTGTGCCCCCTGATATCGGGGCAAGAGGGCGCGCCCAACACCCCGCTCAAC 1687
 Oy 1764 TGCTCCCTGGGAAGTTAAAGGCTGATCATG 1796
 Db 1688 TGCTCCCTGGGAAGTTAAAGGCTGATCATG 1720

RESULT 6
 AF076931
 LOCUS 1716 bp mRNA linear PRI 24-NOV-2000
 DEFINITION Homo sapiens serine/threonine kinase 14 beta (STK14B) mRNA,
 complete cds.
 ACCESSION AF076931
 VERSION AF076931.1 GI:5668906
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1716)
 AUTHORS Lee-Fruman,K.K., Kuo,C.J., Lippincott,J., Terada,N. and Blenis,J.
 TITLE Characterization of S6k2, a novel kinase homologous to S6k1
 JOURNAL Oncogene 18 (36), 5108-5114 (1999)
 MEDLINE 99422045
 PUBMED 10490847
 REFERENCE 2 (bases 1 to 1716)
 AUTHORS Lee-Fruman,K.K., Kuo,C.J., Lippincott,J., Terada,N. and Blenis,J.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUL-1998) Cell Biology, Harvard Medical School, 240
 Longwood Ave., Boston, MA 02115, USA
 FEATURES
 source
 1..1716
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="11"
 /map="11q13"
 /cell_type="Jurkat T cell"
 1..1716
 /gene="STK14B"
 36..1484
 /gene="STK14B"
 /note="similar to p70 S6 kinase; kinase-like S6 kinase;

KLS"
/codon_start=1
/product="serine/threonine kinase 14 beta"
/protein_id="AAD46063.1"
/db_xref="GI:5668907"
/translation="MAAVFDLLETEEGSEGEPELSPADACPLAEPLAEVYGH
VEEVLTEVSANVGERIGPHFELLRLVKGKGYKFEVRRVQGNITIAMVLR
KAKIVRNADTAHTRAEKNILSVKHPFIVELAVAFQVTEGKLYLILEICSGELFTHL
EREGLFLEDTACFYLAELTALAGHLSSOIIYRDLKPENIMLSOGHKLDPGLCKE
SIHEGAVHTFCGTLEYMAPEILVSGHRAVDWMSIGMTDLTGSPFAENRKK
TMDKLIIRGKLALPYLTDPADRLVKKFKLRNPSSOITGGGPGDAAYORHPRHNMMD
DLIARVDPPEPRPCLOSEBDVSGFDTRFRKTPVPSPDPTALSESANOAFLEPTTVAP
SVLDSIKESFSPKLRSPRLNNSPRVPSPLKFSPEGFRPSLSLEPTLPLPLPL
LPPPESTTAPLPPIRPPSGTKSRGRGPR"

BASE COUNT 339 a 532 c 532 g 313 t
ORIGIN

Query Match 94.1%; Score 1708; DB 9; Length 1716;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1708; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY CGACGGGCCCCGGGGCGCCGCGCATGCGGCGCGTGTGATTGATTGGAGAGC 148
DB CGACGGGCCCCGGGGCGCCGCGCATGCGGCGCGTGTGATTGATTGGAGAGC 68
QY 149 GAGGAAGCGCAGGCGGCGAGGCGAGCCAGAGCTCAGCCCGCGGAGCGCATGCCCTT 208
DB 69 GAGGAAGCGCAGGCGGCGAGGCGAGCCAGAGCTCAGCCCGCGGAGCGCATGCCCTT 128
QY 209 GCCGATTTGAGGCGAGCTGCGCTTAGAGCCCTGTGGACACTATGAAGGTGAGCTGACT 268
DB 129 GCCGATTTGAGGCGAGCTGCGCTTAGAGCCCTGTGGACACTATGAAGGTGAGCTGACT 188
QY 269 GAGACCAGCTGTAAGCTGTGGCCAGAGCGCATGCGGCGCCACTGTGCTTGAAGCTGCTGCT 328
DB 189 GAGACCAGCTGTAAGCTGTGGCCAGAGCGCATGCGGCGCCACTGTGCTTGAAGCTGCTGCT 248
QY 329 GTGCTGGGCAAGGGGGGCTATGCGAAGGTGTCAGGTCGGAAGGTGCAAGGCAACCAAC 388
DB 249 GTGCTGGGCAAGGGGGGCTATGCGAAGGTGTCAGGTCGGAAGGTGCAAGGCAACCAAC 308
QY 389 TTGGGGCAAAATATATGCGATGAAGAGTCTTAAGAAAGGCCAAATTTGGCCCATGCCAAG 448
DB 309 TTGGGGCAAAATATATGCGATGAAGAGTCTTAAGAAAGGCCAAATTTGGCCCATGCCAAG 368
QY 449 GACACAGCACACACAGCGGCTGAGCGGCAATCTAGAGTCAGTGAAGCAACCCCTTTATT 508
DB 369 GACACAGCACACACAGCGGCTGAGCGGCAATCTAGAGTCAGTGAAGCAACCCCTTTATT 428
QY 509 GTGGAACCTGGCTATGCTTCCAGACTGTGGCAAACTTACCTCATCTTGAAGTGCCTC 568
DB 429 GTGGAACCTGGCTATGCTTCCAGACTGTGGCAAACTTACCTCATCTTGAAGTGCCTC 488
QY 569 AAGGTGGCGAGGCTTTCCAGGCACTGTGAGCAGAGGAGGCACTTCTTCGGAAGATACGGCC 628
DB 489 AAGGTGGCGAGGCTTTCCAGGCACTGTGAGCAGAGGAGGCACTTCTTCGGAAGATACGGCC 548
QY 629 TGTCTTACCTGCTGATGATCAGCTGCGCTGGGCGCATCTCCACTCCAGGGGCGATCATC 688
DB 549 TGTCTTACCTGCTGATGATCAGCTGCGCTGGGCGCATCTCCACTCCAGGGGCGATCATC 608
QY 689 TACCGGGAGCTCAAGCCGAGAAACATCATCTCAGACGAGGCGCCATCAAACTGAC 748
DB 609 TACCGGGAGCTCAAGCCGAGAAACATCATCTCAGACGAGGCGCCATCAAACTGAC 668
QY 749 GACTTTGAGATCTGCAAGAGAGTCTATCATGAGAGGCGCGCTCATCATCTTGTGGGC 808
DB 669 GACTTTGAGATCTGCAAGAGAGTCTATCATGAGAGGCGCGCTCATCATCTTGTGGGC 728
QY 809 ACCATTGATGATGAGGCGCGCTGAGATTTCTGTGCGAGCTGCGCACACCGGGGCTGTGAC 868
DB 729 ACCATTGATGATGAGGCGCGCTGAGATTTCTGTGCGAGCTGCGCACACCGGGGCTGTGAC 788

QY 869 TGTGTGAGCCTGTGGGGGCGCTGATGTACGACATGCTACTGTGATGCCGCCCTTTACCGCA 928
DB 789 TGTGTGAGCCTGTGGGGGCGCTGATGTACGACATGCTACTGTGATGCCGCCCTTTACCGCA 848
QY 929 GAAACCGGAAAGAAACCATGATGATATCATAGAGGGGCAAGCTGGACATGCCGCCCTTAC 988
DB 849 GAAACCGGAAAGAAACCATGATGATATCATAGAGGGGCAAGCTGGACATGCCGCCCTTAC 908
QY 989 CTGACCCAGATATCCCGGGGCACTTGTCAAAAAGTTTCTGAAAGGAAATCCACAGCCAGCG 1048
DB 909 CTGACCCAGATATCCCGGGGCACTTGTCAAAAAGTTTCTGAAAGGAAATCCACAGCCAGCG 968
QY 1049 ATTGGGGGTGGCCCAAGGGAGTCTGTGATGTGACAGACATCCCTTTTTCGGGCAATG 1108
DB 969 ATTGGGGGTGGCCCAAGGGAGTCTGTGATGTGACAGACATCCCTTTTTCGGGCAATG 1028
QY 1109 AATTGGGAGCAGCTTCTGCGCTGCGCTGGGAGACCCCTTTCAGGCGCTGTGACAGTCA 1168
DB 1029 AATTGGGAGCAGCTTCTGCGCTGCGCTGGGAGACCCCTTTCAGGCGCTGTGACAGTCA 1088
QY 1169 GAGGAGGAGCTGAGCCAGTGTGATACCCGCTTACACAGGCGAGCGCGGTGACAGTCTCT 1228
DB 1089 GAGGAGGAGCTGAGCCAGTGTGATACCCGCTTACACAGGCGAGCGCGGTGACAGTCTCT 1148
QY 1229 GATGACACAGCCTCTCAGCGAGAGTGTCCACACAGCCTTCTGCGCTTACATACGTGGCG 1288
DB 1149 GATGACACAGCCTCTCAGCGAGAGTGTCCACACAGCCTTCTGCGCTTACATACGTGGCG 1208
QY 1289 CCGTCTGTCTGTGACAGCATCAAGAGGGGCTTCTCCAGCGCCAAAGGCGGCTCACCC 1348
DB 1209 CCGTCTGTCTGTGACAGCATCAAGAGGGGCTTCTCCAGCGCCAAAGGCGGCTCACCC 1268
QY 1349 AGGCGCCTCAACAGTAGAGCCCGCGGTCGCCGTCAGGCGCCCTCAAGTTCCTCCCTTTGAG 1408
DB 1269 AGGCGCCTCAACAGTAGAGCCCGCGGTCGCCGTCAGGCGCCCTCAAGTTCCTCCCTTTGAG 1328
QY 1409 GGGTTTGGGCGCAAGCCCGACAGCTGTGGGAGCCACAGGAGCTTACTTCACTCACTCTG 1468
DB 1329 GGGTTTGGGCGCAAGCCCGACAGCTGTGGGAGCCACAGGAGCTTACTTCACTCACTCTG 1388
QY 1469 CCAAGCGGCGCGCGCTGTGACACAGCGCCCTTCCCATCCGCTGCGCCCTCAGGAGACCAAG 1528
DB 1389 CCAAGCGGCGCGCGCTGTGACACAGCGCCCTTCCCATCCGCTGCGCCCTCAGGAGACCAAG 1448
QY 1529 AAGTCCAAGAGGGGCGCTGGGCGTCCAGGGCGCTAGGAAGCCCGGTGGGGGTAGAGGTAG 1588
DB 1449 AAGTCCAAGAGGGGCGCTGGGCGTCCAGGGCGCTAGGAAGCCCGGTGGGGGTAGAGGTAG 1508
QY 1589 CCGTTGAGCCCTGTCCCTGCGGCTGTGAGAGCAGCAGGAGCCCTGGGCGCACTTCCAGAGAC 1648
DB 1509 CCGTTGAGCCCTGTCCCTGCGGCTGTGAGAGCAGCAGGAGCCCTGGGCGCACTTCCAGAGAC 1568
QY 1649 CTGGGGGTGTGTGTGGGGGTGGGGGTGTGAGTGGTATGAAGGTGTGTGTGTGGGGGCA 1708
DB 1569 CTGGGGGTGTGTGTGGGGGTGGGGGTGTGAGTGGTATGAAGGTGTGTGTGTGGGGGCA 1628
QY 1709 GCTGTGCCCCCTGATATGAGGAGCGAGAGGCGCCCGCCACACCCCGCGCTCAACTGCTC 1768
DB 1629 GCTGTGCCCCCTGATATGAGGAGCGAGAGGCGCCCGCCACACCCCGCGCTCAACTGCTC 1688
QY 1769 CCGTGAAGATTAAGGGCTGAATCATG 1796
DB 1689 CCGTGAAGATTAAGGGCTGAATCATG 1716

RESULT 7
AB019245 1744 bp mRNA linear PRI 06-FEB-1999
LOCUS AB019245
DEFINITION Homo sapiens p70 S6kb mRNA for S6 kinase b, complete cds.
ACCESSION AB019245
VERSION AB019245.1 GI:4165310
KEYWORDS p70 S6kb; S6 kinase b.
SOURCE Homo sapiens cell_line:erythroleukemia cell CDNA to mRNA.

QY 1586 TAGCCCTTAGCCCTGTCCTGCGGCTGTGAGACAGACAGACCTTGCGCCAGTTCAGGA 1645
DB 1520 TAGCCCTTAGCCCTGTCCTGCGGCTGTGAGACAGACAGACCTTGCGCCAGTTCAGGA 1579
QY 1646 GACCTGGGGGTGTGTCTGGGGGTGGGGGTGTGACGTGTATGAAGTGTGTCTGGGG 1705
DB 1580 GACCTGGGGGTGTGTCTGGGGGTGGGGGTGTGACGTGTATGAAGTGTGTCTGGGG 1638
QY 1706 GACAGCTGTGCCCCCTGATCATCTGGGACAGGAGGCGCCGCCACACCCCGCTCAACTG 1765
DB 1639 GCAAGCTGTGCCCCCTGATCATCTGGGACAGGAGGCGCCGCCACACCCCGCTCAACTG 1698
QY 1766 CTCCTGCGGAAGATTAAAGGCGCTGATCATGAAAAA 1808
DB 1699 CTCCTGCGGAAGATTAAAGGCGCTGATCATGAAAAAAGGAA 1741

RESULT 8
LOCUS MMU7938 1491 bp mRNA linear ROD 20-NOV-1998
DEFINITION Mus musculus S6 kinase 2.
ACCESSION AJ007938
VERSION AJ007938.1 GI:3901074
KEYWORDS S6 kinase 2; S6K2 gene.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
1 (bases 1 to 1491)
Kozma, S.C.
Direct Submission
Submitted (15-JUL-1998) Kozma, S.C., Growth Control, Friedrich Miescher Institute, P.O. box 2543, Basel, CH-4002, SWITZERLAND
REMARK 2 (bases 1 to 1491)
Shima, H., Pende, M., Chen, Y., Fumagalli, S., Thomas, G. and Kozma, S.C.
Distribution of the p70(S6K)/p85(S6K) gene reveals a small mouse phenotype and a new functional S6 kinase
EMBO J. 17 (22), 6649-6659 (1998)
JOURNAL 99043870
MEDLINE 9822608
PUBMED
FEATURES
source location/Qualifiers
1..1491 /organism="Mus musculus"
/db_xref="taxon:10090"
1..1458 /gene="S6K2"
1..1458 /gene="S6K2"
/gene="S6K2"
/codon_start=1
/product="S6 kinase 2"
/protein_id="CA07774.1"
/db_xref="GI:3901075"
/translation="MAAVPDLIEETEGSEGEPEFSPADVCPLGELAAQLETYGH
YEVVELTSSVNDLPERIGPHCEFLISVJGKGTVGVFVRYQGNLKIYAMKLR
KAKIVCSANDTAHTAERNILSVKHPFLVEAYATGKLYLILECLSGELFTHL
EBEGIFLEDYACFYLAETILALGHLSHQIYRDLPENIMLSQGHILTFGLCKE
SIHEGATITFCGTIEYMAPEILVTRGHNRADVMELGALMDMLGSPPTAENRK
TMDKITKGLVLPYLTLPDARDLAKKELRNPTORTGGIGLGAADVQRHPFPHIWD
DLARVPDPSPRLOSIEDVQOFDARFTRQTPYDSDPTALSESNAQFLGTYAP
SYLDSIKESFSPDKLRSFRLNSPRTISPLKTSFFRGFRSPGPPPEMPSLPPL
LPSPSPPTSTAPLPIRPSPGTRKSKRGGRGR"

BASE COUNT 358 a 436 c 403 g 294 t
ORIGIN

Query Match 64.0%; Score 1161.6; DB 10; Length 1491;
Best Local Similarity 87.8%; Pred. No. 6.8e-224;
Matches 1282; Conservative 0; Mismatches 169; Indels 9; Gaps 1;

QY 116 ATGGCGGCGCTGTTGATTGATTGAGACGAGAGGAGGAGGCGGCGAGGCGAG 175
DB 1 ATGGCGGCGCTATTGATTGATTGAGACTTGAGACGAGAGGAGGAGGCGGCGAG 60

QY 176 CAGAGCTCAGCCCGCGGACGACATGTCCTCTGCGAGTTGAGGCGAGCTGGCTAGAG 235
DB 61 CCGAGATTGACCCCTCGCGACGTGTCTCTGCGGAATTAAGGCGCTGCGCTGGAG 120
QY 236 CCGTGGGACATATGAAGGTGGAGCTGACGTGAGACCGAGCGGTGAACGTTGGCCAGAG 295
DB 121 ACAGTGGACATATGAAGGTGGAGCTGACGTGAGACCGAGCGGTGAACGTTGGCTGAG 180
QY 296 CCGATGGGCGCCCACTGCTTTGAGCTGCTGCTGCTGCTGGGCAAGGGGGCTATGGCAAG 355
DB 181 CGCATGGGCGCCCACTGCTTTGAGCTGCTGCTGCTGCTGGGCAAGGGGGCTATGGCAAG 240
QY 356 GTGTTCAGCTGCGGAAGGTGCAAGGACCACTTGGGCAAAATATATGCTAGAAAGTC 415
DB 241 GTGTTCAGCTGCGGAAGGTGCAAGGACCACTTGGGCAAAATATATGCTAGAAAGTC 300
QY 416 CTAAAGGAGGCGCAAAATTTGGCGCAATGGCAAGGACACACACAGCGGCTGAGCGG 475
DB 301 TTAAGGAGGCGCAAAATTTGATGACAGTGGCAAGGACACACCGCTGAGAGG 360
QY 476 AACATTCTAGAGTCAGTGAAGACACCCCTTATTTGTGGAACTGGGCTATGCTTCAGACT 535
DB 361 AACATTCTAGATCTGTGAAGACATCCCTTATTTGTGAAGTGGGCTATGCTTCAGAGCA 420
QY 536 GTGTGCAACTTCACTCATCTTGAAGTGGCTGAGTGGGCGAGCTTTCACGCAATCTG 595
DB 421 GTGTGCAACTTCACTCATCTTGAAGTGGCTGAGTGGGCGAGCTTTCACGCAATCTT 480
QY 596 GAGCGAGAGGCGCATCTTCTGGAAGATACGCGCTGCTTACCTGGCTGAGTACAGCTG 655
DB 481 GAGCGAGAGGCGCATCTTCTGGAAGATACGCGCTGCTTACCTGGCTGAGTACAGCTG 540
QY 656 GCCCTGGGCGCATCTTCACTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 715
DB 541 GCCCTGGGCGCATCTTCACTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
QY 716 ATGCTCAGACGACGAGGCGCACATCAAACTGACCGACTTTGGACTTGCAGAGTCTATC 775
DB 601 ATGCTCAGACGACGAGGCGCACATCAAACTGACCGACTTTGGACTTGCAGAGTCTATC 660
QY 776 CATGAGGCGCGCTCATCTGACACCTTCTGGGAGACATTAAGTATGAGGCGCTGAGATT 835
DB 661 CATGAGGCGCGCTCATCTGACACCTTCTGGGAGACATTAAGTATGAGGCGCTGAGATT 720
QY 836 CTGCTGCGAGTGGCGCAACCGGCGTGTGAGCTGTGAGACCTTGGGCGCTGATGTAC 895
DB 721 CTAGTGGCGACTGTGTACAAACGGGCGAGTGTGAGTGTGAGGAGGCGCTGATGTAC 780
QY 896 GACATGCTCACTGATGCGCGCGCTTACCGGACAGAACCGGAAGAAACATGATTAAG 955
DB 781 GACATGCTCACTGATGCGCGCGCTTACCGGACAGAACCGGAAGAAACATGATTAAG 840
QY 956 ATATCAGGGGCGCAAGCTGGGACGACGCGCGCTTACTCAACCCCAATGCGGGGACCTTGC 1015
DB 841 ATATTAAGGGAAGAGGTGGTGTGCGCGCGCTTACTCAACCCCAATGCGGGGACCTTGC 900
QY 1016 AAAAAGTTTGTGAAGGAAATCCACGACGAGGATTGGGGGTGGCCAGGAGTGTGCT 1075
DB 901 AAAAAGTTTGTGAAGGGAACCCACACTCAGCAGGAATTGGGGGTGGCCAGGAGTGTGCT 960
QY 1076 GATGTGACAGACATCCCTTTTCCGCGACATGAATTTGGAGCAGCACTTCTGCGCTGGCT 1135
DB 961 GATGTGACAGACATCCCTTTTCCGCGACATGAATTTGGAGTATGATCTTGGCCGCGCGC 1020
QY 1136 GTGAGCCCGCTTTCAGGCGCTGTGACAGTCAAGAGAGGAGGAGGAGGAGGAGGAGGAG 1195
DB 1021 GTGAGCCCTTCTTCAGGCGCAAGTGTGCAATCAAGAGAGGAGTGTGAGGAGGAGGAG 1080
QY 1196 CGCTTCACAGGAGAGGCGGCTGGACAGTCTGATGACACAGCCCTCAGCGAGAGTGC 1255
DB 1081 CGATTTCACAGGAGAGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 1256 AACGAGGCTTCTCTGGGCTTCAATACATGAGTGGCGCGCTGTCTCTGGAACAGATCAAGAG 1315

Db	1141	AACCAAGCCTTCGAGGGCTTACATATGTGGACCTCTGTGCTGTGGACAGCATCAAG	1200
Qy	1316	GGCTTTCCTTCCAGACCCAAAGCTGGCTGACCCAGGCGCTTCACAGTAGCCCCGGGTC	1375
Db	1201	GGCTTTCCTTCCAGGCCCAAGCTGGCTTCCCAAGACGCTTAACAGCAGTCCCGGACGC	1260
Qy	1376	CCGGCAGCGCCCTCAATGTCCTCCCTTTAGGGGTTTGCCGCCAGGCCCAAGCCTGGCG	1435
Db	1281	CCCATACAGCCCTCAATGTCCTCTGCTTTAGGGGTTTGCCGCCAGTCCGGGCCACCA	1320
Qy	1436	GAGCCACAGGAGTACCTCTACCTCACTGCT-----GCCACCGCGCGCGGCGCTCG	1486
Db	1321	GAGCGCAGTAGGCATCTCTACCTCACTGCTTCACTCAATCACCACCATTCACACCAACCA	1380
Qy	1487	ACCAACGCGCTCTGCCATCGTCGCCCTTCAGGGACCAAGAAAGTCCAAAGAGGGCGGT	1546
Db	1381	AGCACTGCGCCCTTCTCCATCGTCTCCCTCAGGAACAAGAAAGTCCAAAGAGGGACGG	1440
Qy	1547	GGGGGTCCAGGGCGCTAGGA	1566
Db	1441	GGCGGCTCAGGGCGCTTAGGA	1460

LOCUS	AR086879	1607 bp	DNA	linear	PAT 07-SEP-2000
DEFINITION	Sequence 4 from patent US 5985635.				
ACCESSION	AR086879				
VERSION	AR086879.1	GI:10013645			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1607)				
TITLE	Bandman,O., Goll,S.K. and Hillman,J.L.				
JOURNAL	Nucleic acids encoding novel human serine/threonine protein kinases				
FEATURES	Patent: US 5985635-A 4 16-NOV-1999;				
source	Location/Qualifiers				
	1..1607				
	/organism="unknown"				
BASE COUNT	312 a	519 c	472 g	283 t	21 others
ORIGIN					
Query Match	39.6%; Score 720; DB 6; Length 1607;				
Best Local Similarity	99.1%; Pred. No. 5.4e-15;				
Matches 734; Conservative	0; Mismatches 6; Indels 1; Gaps 1;				
QY	874	GAGCGTGGGGGCGCTGATGTCAGACATCTCAGTGGATCCGCCCTTTACCGCAGAGAA	933		
DB	868	GCGCGTGGGACCGCTGATGTCAGACATCTCAGTGGATCCGCCCTTTACCGCAGAGAA	927		
QY	934	CCGGAGAGAAACCATGATGATGATCAGGAGGCAAGTGGGACAGCCCTTACCTCAGC	993		
DB	928	CCGGAGAGAAACCATGATGATGATCAGGAGGCAAGTGGGACAGCTTACCTCAGC	987		
QY	994	CCAGATGCCCGGGGACCTTGTCAAAAAGTTTCTGAAAGGGAATCCAGCAGCGGATTGG	1053		
DB	988	CCAGATGCCCGGGGACCTTGTCAAAAAGTTTCTGAAAGGGAATCCAGCAGCGGATTGG	1047		
QY	1054	GGGTGGCCCAAGGGATGCTGCTGATGTCAGAGACATCCCTTTTCCGGCACATGAATG	1113		
DB	1048	GGGTGGCCCAAGGGATGCTGCTGATGTCAGAGACATCCCTTTTCCGGCACATGAATG	1107		
QY	1114	GGAGACCTTTCGGGCTGGCGTGGGAGACCCGCTTTCAGGGCCCTGTGCAATGAGAGA	1173		
DB	1108	GGAGACCTTTCGGGCTGGCGTGGGAGACCCGCTTTCAGGGCCCTGTGCAATGAGAGA	1167		
QY	1174	GGAGGTGAGCCAGTTTGTATACCCGCTTTCACAGGAGAGCGCGGTGGAGAGCTGATGA	1233		
DB	1168	GGAGGTGAGCCAGTTTGTATACCCGCTTTCACAGGAGAGCGCGGTGGAGAGCTGATGA	1227		
QY	1234	CACAGCCCTTCAGCGAGAGATGCCAACAGGCGCTTCCTGGGCTTCACATGATGTTGGCCGTC	1293		

Db	1228	CACAGCCCTTCAGGCGAGATGGCAACCAAGGCCCTTCCTGGGGCTTCACATFAGTGGGCGCGTC	1287
QY	1294	TGTCTGGACACGATCAAGGAGGGCTTCTCTTCCAGGCCAAAGCTGCGCTACCCAGGCG	1353
Db	1288	TGTCTGGACACGATCAAGGAGGGCTTCTCTTCCAGGCCAAAGCTGCGCTACCCAGGCG	1347
QY	1354	CCTCAACAGTAGACCCCGGGGCCCGGTACAGCCCTCAAGTCTCCCTTTGAGGGGT	1413
Db	1348	CCTCAACAGTAGACCCCGGGGTCCCGGTACAGCCCTCAAGTCTCCCTTTGAGGGGT	1407
QY	1414	TGGGCCAGCCCCAGCCCTGCGGGAGCCCAAGGAGGCTACCTTCACTCTCGCCAC	1473
Db	1408	TGGGCCAGCCCCAGCCCTGCGGGAGCCCAAGGAGGCTACCTTCACTCTCGCCAC	1467
QY	1474	GCGCGCGCCCTGACACACGCGCCCTCTGCCATTCGTCGCCCTCTAAGGAGACCAAGAGTC	1533
Db	1468	GCGCGCGCCCTGACACACGCGCCCTCTGCCATTCGTCGCCCTCTAAGGAGACCAAGAGTC	1527
QY	1534	CAAGAGGGGCGGTGGGCGTCCAGGGCGGTAGGAACCGGGGTGGGGGTAGAGGTAGCCCTT	1593
Db	1528	CAAGAGGGGCGGTGGGCGTCCAGGGCG- TAGGAACCGGGGTGGGGGTAGAGGTAGCCCTT	1586
QY	1594	GAGCCCTGCTCCCTGGGCGCT	1614
Db	1587	GAGCCCTGCTCCCTGGGCGCT	1607

LOCUS	1800 bp	mRNA	linear	ROD 27-APR-1993
DEFINITION	RATS6KIN3			
VERSION	Rat S6 kinase mRNA, complete cds.			
KEYWORDS	M57428 M3864			
SOURCE	M57428.1 GI:206839			
ORGANISM	S6 kinase.			
	Rat (strain Sprague-Dawley) liver, cDNA to mRNA.			
	Rattus norvegicus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
REFERENCE	1 (bases 1 to 1800)			
AUTHORS	Kozma,S.C., Ferrarli,S., Bassand,P., Siegmann,M., Totty,N. and Thomas,G.			
TITLE	Cloning of the mitogen-activated S6 kinase from rat liver reveals an enzyme of the second messenger subfamily			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 87 (19), 7365-7369 (1990)			
MEDLINE	91017506			
PUBMED	1699226			
REFERENCE	2 (sites)			
AUTHORS	Lane,H.A., Morley,S.J., Doree,M., Kozma,S.C. and Thomas,G.			
TITLE	Identification and early activation of a Xenopus laevis p70s6k following progesterone-induced meiotic maturation			
JOURNAL	EMBO J. 11 (5), 1743-1749 (1992)			
MEDLINE	92258384			
PUBMED	1374712			
FEATURES	Location/Qualifiers			
SOURCE	1..1800			
	/organism="Rattus norvegicus"			
	/strain="Sprague-Dawley"			
	/db_xref="taxon:10116"			
	/tissue_type="liver"			
	/dev_stage="7-8 week"			
	/tissue_1lb="stratagene lambda zap II 936507"			
	1..1800			
	/gene="S6 kinase"			
	134..1642			
	/gene="S6 kinase"			
	/codon_start=1			
	/product="S6 kinase"			
	/protein_id="AA42103.1"			
	/db_xref="GI:206840"			
	/translation="MAGVFDDLDQPEDAGSEDELEEGQINSMADHGCVGPEYLGNHCEFFSETSVNGPEKIRPECCFLRLVLQGGYGRVQRYKVTGANTGIFPMKTVL			

Db	73	CACAGGGAGACCTGAGGACATGCGAGGAGGTGTTGACATATGACCTGGACACGACAGAGAT	132
Oy	158	AGCGAGGGCAGAGCGCAGCCAGACTCAGCCCCCGGAGCGATGTCCTTGGCGAGTTG	217
Db	133	GCAGGCTCTGAGATGAGCTGCGAGGAGGGGGGTGCAATTAAATGAAGCATGGACCATGGG	192
Oy	218	AGGGCAGCTGGCTAGACCTG --- -TGGGACACATATGAAGAGTGGACCTGACTGAGACC	274
Db	193	GGATTTGGACCATATGAACTTGGCAATGGAAACATTTGGAAATTTGAAATCTCAGAAACT	252
Oy	275	AGCCTGAACCTTGGCCAGAGCCCATCGGAGCCCACTGCTTGGACCTCTCGATGTGCTG	334
Db	253	AGTGTGAACAGAGGGCCAGAAAAATCAGACCAGATGTTTTGACACTACTTCGGGTACTT	312
Oy	335	GGCAAGGGGGCTATGGCAGAGTGTTCAGGTGCGAAAGTGCAGACGACCACTTGGGC	394
Db	313	GGTAAAGGGGGCTATGGAAAGGTTTTTCAAGTAAACAGGAGCAAAATCTGGG	372
Oy	395	AAATATATCCCATGAAAGTCTTAAGGAAGCCAAATTTGTCCGATATCCAGAGACACA	454
Db	373	AAGATATTTCCCATGAAGGGTCTTAAAGAGCAATGTATGTAAAGAAATCTAAAGATACA	432
Oy	455	GCACACACAGGGGCTGAGCGGCAATCTTAAGATCAGTAACACACCCTTTATTTGGA	514
Db	433	GCTATATCAAAAGACAGAGCGGAAATTTCTGGAGGAAGTAAACATCTCCTTCACTTGTGAT	492
Oy	515	CTGGCCTATGCTTCACGACTGGTGGCAAACTCTACCTCATCTTGAAGTGCCTAGTGT	574
Db	493	TTAATTTATGCTTCAGACCCGGTGGAAACTCTACCTCATCTTGAATCATGTGGA	552
Oy	575	GGCCAGCTCTTACAGCATCTGGAGCGAGAGGCATCTTCTTGGAAATACGGCTGCTTC	634
Db	553	GGAGAACTATTATTAGCGATTAGAAAGAGAGGGATTTTCATGGAAGATACACACTTGTCTT	612
Oy	635	TACCTGGCTGATCAGCTGCTGGCCCTGGGCACTCTCCATCCGAGGCATCTTACCGG	694
Db	613	TACTTGGCTGAATCTCCATGCGCTTTTGGGCAATTTACATCAAAAGGGATTATCTACGA	672
Oy	695	GACCTCAAGCCCGAAGCATCATGCTCAGAGGCCAGGGCCACATCAAACTGACGACTTT	754
Db	673	GACCTGAAGCCGGAGACATCATGCTTTAATCACCAAGTCACTGTAAGCTGACAGACTTT	732
Oy	755	GGACTCTGCAGAGAGTATATCCATGAGGGCGCCGTACTCTACACCTTCTCGCGCACCTT	814
Db	733	GGACTATGCAAAAGATATCTTATCAATGATGAGAACGTCCACCAACATTTTGTGGAAACATA	792
Oy	815	GAGTACATAGGCCCCGTGATTCGTGGCGAGTGGCGCAACACCGGGCTGGACGTGGG	874
Db	793	GAATATCATGGCCCCGTGAATCTTGATATGAGAAAGGGCCACACCGCTGTGGATTGGTG	852
Oy	875	AGCCTGGGGGCCCTGATGATGACGATGCTACATGATGCGCCGCCCTTATACCGCAGAGAC	934
Db	853	AGTCTGGGAGATTTAATGTATGACATGCTGACCTGGAGCACCTCCATCTACTCTGGGAGAT	912
Oy	935	CGAAGAAAACCATGATTAAGATCATAGGGGCAAGCTGGCACTGCCCCCTTACTCTACC	994
Db	913	AGAAAGAAAGACAAATTGACAAATCTCATAATGTAACCTTAATTTGGCTCTCCACTCACA	972
Oy	995	CCAATGCTCCCGGAGCTTGTCAAAAAGTTTCTAACCAGAAATCCAGCGAGGATTTGGG	1054
Db	973	CAGAGAGCTCAGATGTGCTTTAAAGAGCTGTAAAGAAATGTGCTTCTGTCTTGGGA	1032
Oy	1055	GGTGGCCAGAGGATGCTGCTGATATGTCAGAGACATCTCTTTTTCGCGACATGAATTGG	1114
Db	1033	GCTGGCCCTGGGGATGCTGTGAGAGATCCAAAGCGCATTCATTTTTTATGACACATTTAACTGG	1092
Oy	1115	GACGACCTTCTGGCTGGCGTGGAGCCCCCTTTCAGGCCCCGTGCTGCAGTCAAGAGAG	1174
Db	1093	GAAAGACTTTTGGCTCGGAAGGTGAGACGCCCTTAAACCTCTGTGTGAATCTGAAG	1152
Oy	1175	GACGTGAGCCAGTTTGAATACCCGCTTACACAGGCACAGCGCGGTGGACAGTCTCATATAC	1234
Db	1153	GATGTAGATCGTTTGAATCAAGTTTATCTGTCACACACCTGTGTGACAGCCCCGATATTC	1212

QY	1235	ACAGCCCTCAGGAGAGAGCCCAACACGAGCCCTTCCGCGCTCACATACGAGCCGCTCT	1294
DB	1213	TCACACTCTCAGTGAAGAGTCCCAACCAAGGCTCTTTCGCGTTTACATATAGTGCGTCAATCT	1272
QY	1295	GTCTCTGACAGCATCCAGAGGAGGCTTCTCTCTCCAGCCCAAGCTCGCTCAACCCAGGCGC	1354
DB	1273	GTACTTGAAGAAGTGTGAAGAAAGATTTCTTTCTTTGAACCAAAATTCGATCGCTCGAAGA	1332
QY	1355	CTCAACAGTAGCCCCCGGGGTCCGCTCAGGCCCTCAAGTTCTCCCTTTTGA	1407
DB	1333	TTTATTGGTAGCCCAAGAACGCTGTCAAGCCAGTCAATTTCTCTCGGGGA	1385
RESULT 12			
OCG3PK			
LOCUS			
DEFINITION	OCG3PK	1778 bp	MRNA
ACCESSION	Rabbit mRNA for serine/threonine kinase homologous to ribosomal		MAM 10-JAN-1991
VERSION	protein S6 kinase.		
KEYWORDS	X54415		
SOURCE	X54415.1 GI:1561		
ORGANISM	protein kinase; serine threonine kinase.		
REFERENCE	Oryctolagus cuniculus.		
AUTHORS	Oryctolagus cuniculus		
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
JOURNAL	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
REFERENCE	1 (bases 1 to 1778)		
AUTHORS	Killmann, M.W.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-AUG-1990) Killmann M.W., Institut fuer Physiologische		
REFERENCE	Chemie, Universitaet Bochum, Postfach 10 21 48, D-4630 Bochum 1,		
AUTHORS	FRG		
TITLE	2 (bases 1 to 1778)		
JOURNAL	Harmann, B. and Killmann, M.W.		
REFERENCE	cDNA encoding a 59 kDa homolog of ribosomal protein S6 kinase from		
AUTHORS	rabbit liver		
TITLE	FEBS Lett. 273 (1-2), 248-252 (1990)		
JOURNAL	91032193		
MEDLINE	1699810		
PUBMED			
FEATURES			
source	Location/Qualifiers		
MRNA	1..1778		
CDS	/organism="Oryctolagus cuniculus"		
	/db_xref="taxon:9986"		
	/clone="G3"		
	<1..1778		
	28..1605		
	/codon_start=1		
	/product="G3 serine/threonine kinase"		
	/protein_id="CAA38279.1"		
	/db_xref="GI:1562"		
	/db_xref="SWISS-PROT:P21425"		
	/translation="MRRRRRGGGYPADPFEDPREAAGVFDIDIDPQEDAGSEDEL		
	EEGGGLNDSMDHGCVPELCEHCEKEKEISETSYNNRPEKIREPCBELLVLDKGGT		
	EGKIVRRVVTGANTGKIFAMKVLAAMVVRNAKDTAHTKAEKNILLEEYKPFIVDLITY		
	AFQEGKLYLILEYLSGGELEFMOLEREQIFEMEDACFTLAEISALGHLHQKGIYRDL		
	LKPEHMLNHOGHVKLIDPFGLESIRREGIETVHTFCGIIEYMAEILMRSGHNRAVDVW		
	WSIGALMTDMLTGAAPPTGENRRTIKLILCKNLNLPYLQEARDLKILKRNAAAS		
	RIGAGRGDAGVOAHPFRPHNIMELLARVKEPKYKPLIOSEEDVSDPSKFTROTPTV		
	DSPPDSTISBANOVFLCFTTVAASVLESVKEKTSFEKINSPPRFISPTPIVSPYKAK		
	FSPDGFWERGASASTANPOTPEVEYPMETSGIEMDVTTSGEASAPLPIROPNSPYKKK		
	QAFPMISKRPRLRNLT"		
	28..1602		
	/product="G3 serine/threonine kinase"		
	1778		
BASE COUNT	555 a	361 c	457 g 405 t
ORIGIN			
polya_site			
Query Match	34.1%;	Score 619.8;	DB 4; Length 1778;
Best Local Similarity	70.5%;	Pred. NO. 8e-115;	
Matches 824;	Conservative 0;	Mismatches 344;	Indels 0;
Gaps 0;			
QY	240	TGGGACACTATGAGAGAGTGTGAGCTGTGAGACAGCGTGAACGTTGGCCCAAGAGCGCA	299


```

Db      363  AATATTTCCATGAAAGGCTTAAAGCAATGATAGTAAAGAAATGCTAAAGATACAGC  442
Oy      457  ACACAGCGGGCTGAGCAATCTAGAGTCAGAGGACCGCTTATTTAGTGGACT  516
Db      443  TCATACAAAGACGAAACGGAATTTCTGAGAGAAATTAAGATCCCTTCATGTGTGATTT  502
Oy      517  GGCCTATGCTTCAGACTGTGTGCAAACTTACTCATCTCTGAGTGGCTCATGTGTG  576
Db      503  AATTATGCTTTCAGACTGTGTGAAATCTTACTCATCTCTGAGTATCTCATGTGTGAG  562
Oy      577  CGAGCTTTCACGATCTGTGAGAGGAGGACCTTCTCTGAGATACGCGCTGCTTCTA  636
Db      563  AGAATATTTATGCACTTAAAGAGAGGAAATATTTATGGAAGACACTGCTGCTTTTA  622
Oy      637  CCTGCTAGATACGAGTGGGCGCTTCCAGCTCCAGGCGATCATCTACCGGGA  696
Db      623  CTTGGCAAAATCTCATGAGGCTTGGGCAATTTACATCAAAAGGGGATCATCTACAGAGA  682
Oy      697  CCTCAAGCCCGAGAACATCATGCTCAGACAGCGGCGCCACATCAAACTGACCGACTTGG  756
Db      683  CCTGAGCGCGGAGATATCATGCTTAAATCCAGAGTCAATGAAACATCAAGACTTTGG  742
Oy      757  ACTCTGCAAGAGATCTATCCATGAGGCGCGCTCACTACACCTTCTGCGGCAACCATTTGA  816
Db      743  ACTATGCAAAAGAAATCTATTCATGATGAAACAGTCAACACATTTTGTGAAACAATAGA  802
Oy      817  GTACATGGCCCTCGATTTCTGTGCGCAGATGCGCAACACCGGCGTGTGAGTGTGTGG  876
Db      803  ATACATGGCCCTCGAATCTTGATGAGAGTGGCCCAATCTGTGTGATTTGTGTGGAG  862
Oy      877  CTTGGGCGCCCTGATGTACGACATGCTCACTGATGCGCGCCCTTTACCGCAGAAACCG  936
Db      863  TTTGGAGCATTAATGTATGACATGCTGACTGAGACACCCCATTCACAGGGGAGAAATAG  922
Oy      937  GAAGAATACATGATTAAGATCATAGGGGCAAGCTGCGACTGCCCCCTTACTTCAACCC  996
Db      923  AAAGAAACAAATTTGACAAATCTCAAAATGTAACTCAATTTGCTCCCTACTCACAACA  982
Oy      997  AGATGCGCGGACCTTGTCAAAAGTTCTGAAAGGAAATCCACACCGAGGATTTGGGG  1056
Db      963  AGAAGCCAGAGATCTGCTTAAAGAGCTGCTGAAAGAAATGCTGCTTCTGCTGTGGAGC  1042
Oy      1057  TGGCCAGAGGAGTGTGCTGATGTGACAGACATCCCTTTTCCGCAACATTAATTTGGA  1116
Db      1043  TGGTCTGGGAGCGCTGGAGAACTTCAAGCTCATCTTTTAACACATTAATTTGGA  1102
Oy      1117  CGACCTTGTGCGCTGCGCTGTGAGACCCCTTTCAAGCCCTGTGCTGAGTGTGAGAGAGA  1176
Db      1103  AGAATCTTGTGCTCGAAAGGTGAGCCCTTTAAACCTGTGTCATCTGAAAGAGA  1162
Oy      1177  CGTGAGCCATTTGATTAACCCGCTTCAACAGGAGACGCGGTGAGACAGTCTGATGACAC  1236
Db      1163  TGTAACTAGATTTGATTTCAAGTTTACAGTCAACCTGTGACAGGCGAGATGACAC  1222
Oy      1237  AGCCCTCAGAGATGTGCAACAGGCGCTTCTGAGGCTTCAATCATGTGTGCGCGCTGT  1296
Db      1223  AACTCTAGTGAATGTGCAATCAGAGTCTTCTGGGTTTAAATATGTGTGCTCATGT  1282
Oy      1297  CCTGACAGCATCAAGAGGCGCTTCTCTCCAGCCCAAGCTGCGCTCACCCAGCGCGCT  1356
Db      1283  ACTTGAAGTGTGAAGAAATTTTCTTGAACCAAAATTCGATCACCTGCAAGATTT  1342
Oy      1357  CAAGCTAGCCCCCGGGTCCCGTACAGCCCTCAAGTTCTCCCTTTTGA  1407
Db      1343  TATTGGACGCCACGAAACACCTGTCAAGCCCAATTTTCTCTGGGGA  1393

```

```

RESULT 14
AX333655
LOCUS     AX333655      2346 bp    DNA          linear    PAT  09-JAN-2002
DEFINITION Sequence 4164 from Patent WO0194629.
ACCESSION AX333655

```

```

VERSION   AX333655.1  GI:18124374
KEYWORDS
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
           Horigan,S., Soper,D.R. and Weaver,Z.
TITLE      Cancer gene determination and therapeutic screening using signature
           gene sets
JOURNAL    Patent: WO 0194629-A 4164 13-DEC-2001;
FEATURES
source     1..2346
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
BASE COUNT 750 a 453 c 558 g 585 t
ORIGIN
Query Match      34.1%; Score 619.8; DB 6; Length 2346;
Best Local Similarity 70.5%; Pred No. 7.8e-115;
Matches 824; Conservative 0; Mismatches 344; Indels 0; Gaps 0;
Oy      240  TGGGACACTATGAAAGAGTGTGAGTGTGAGAGACGAGCCAGCGTGGCCAGAGCGCA  299
Db      224  TGGAACTGTGTGAGAAATTTGAAATCTCAGAAACTAGTGTGAACAGAGGCCAGAAAAA  283
Oy      300  TCGGGCCCCACTGTCTTTGAGCTGTGCTGTGCTGTGGGCAAGGGGGCTATGGCAAGTGT  359
Db      284  TCGAGACAGAAATGTTTGTGAGTCTCTGCGGTACTTGTGTAAAGGGGCTATGGAAAGGTTT  343
Oy      360  TCCAGGTGTGAAAGGTCAGACACCAACTTGGGCAAAATATGTCATGAAAGTCTTAA  419
Db      344  TTCAAGTACGAAAGTAAACAGAGCAAAATCTGGGAAATTTGTGCATGAAAGTGCTTA  403
Oy      420  GGAAGGCCAAATTTGTGCGCAATGCGCAAGGACAGACACACAGCGGCTGTGAGCGAACA  479
Db      404  AAAAGCAATGATGATGAAGAAATGCTAAAGATACAGCTCATACAAAGCGAAGCGAATA  463
Oy      480  TTCTAGAGTCACTGAAAGCACCCCTTTATTTGTGGAACGTGCGCTATGCTTCCAGCTGTG  539
Db      464  TTTCTGAGAGAAATGAAGCAATCCCTTCATCTGATTTAAATTTATGCTTTTCAGACTGTG  523
Oy      540  GCAACTCTACTCATCTCTGAGTGTGCTGCTGAGTGTGAGGAGGCGTCTCAAGCATCTGAGAC  599
Db      524  GAAACTCTACTCATCTCTGAGTGTGCTGAGTGTGAGGAGGAGTGTGAGTGTGAGTGTGAG  583
Oy      600  GAGAGGCGATCTTCTGGAAGATAGGCGCTGCTTACTCTGAGTGTGAGTGTGAGTGTGAG  659
Db      584  GAGAGGGAATATTATGGAAGACACTGCTGCTTTTACTTGGCAGAAATCTCATGAGCTT  643
Oy      660  TGGGCAATCTCCATCTCCAGGCGATCATCTTACCGGAGCTCAAGCCCGAAGCATCATGTC  719
Db      644  TGGGCAATTTACATCAAAAGGGGATCATCTACAGAGACTGTGAAGCCGCGGAATATATGTC  703
Oy      720  TCAGAGCGAGGCGCAACATCAAGTCAAGGAGCTTTGAGTGTGAGTGTGAGTGTGAGTGTG  779
Db      704  TTAATCACCAAGGTATGTGAAATCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG  763
Oy      780  AGGGGCGCTCACTACACATCTTCTGCGGACCATTTGAGTGTGAGTGTGAGTGTGAGTGTG  839
Db      764  ATGGAACAGTCAACACACATTTTGTGGAACAATGAAATATGAGTGTGAGTGTGAGTGTG  823
Oy      840  TGGCGATGTGCGCAACAACGGGCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG  899
Db      824  TGAGAAAGTGGCCACAATGTGCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG  883
Oy      900  TGGCTACGTGATGCGCGGCTTTACCGGAGAGAACCGGAAACCATGATTAAGATA  959
Db      884  TGTCTACTGTGAGACCCCATTCCTGAGGAGAAATGAAGAAACAAATTTGCAAAATTC  943
Oy      960  TCAGGGGCAAGCTGTGCACTGCCCCCTTACTTCACCCAGAGATCCCGGAGCTTGTCAAAA  1019

```

Db 944 TCAATGTAACGTAATTTGGCTTCCTACCTCAGACAGAGGACAGATCTGCTTAAAA 1003
QY 1020 AGTTTCTGAAGAGGAATCCAGCAGCGATTTGGGGTGGCCAGGGAGATGCTGTGATG 1079
Db 1004 AGCTGCTGAAAAAATGCTGCTTCGTCTGTGGAGCTGTCTCTGGGACGCTGGAGAAAG 1063
QY 1080 TGCAGAGACATCCCTTTTTCGGGACATGAAATTGGAGACACCTTCGTGGCCGTGGCTGTG 1139
Db 1064 TTCAAGCTCATTCATCTTATAGACATTAATCTGGGAAGAACTTGTGGCTGAAAGGTGG 1123
QY 1140 ACCGCCCTTCAGAGCCCTGCTCAGAGTCAGAGAGACGTCGACGATTTGATACCCGCT 1199
Db 1124 AGGCCCTTTTAAACCTCTGTGTCATCTGAAAGAGATGTAACATGATTTGATTTCCAAAGT 1183
QY 1200 TCACAGGAGAGAGCGGCTGGAGATGCTGATGACACAGCCCTCAGCGAGAGATGCCAAC 1259
Db 1184 TTACAGCTCAGACACCTGTGACAGCCAGATATGATCACTCAGAGAAAGTGCACATC 1243
QY 1260 AGGCTCTTCCTGGCTTCACATTCAGTCGGCGGCTGTCTCTGACACAGCATCAAGAGGCT 1319
Db 1244 AGGTCTTCTGGCTTTTACATATGATGTGGCTCATCTGATCTGAAAGTGAAGAAAGT 1303
QY 1320 TCTCCTTCAGCCCAAGCTGCGCTCACCCAGGGCCCTCAGACATAGCCCCGGGTCCCG 1379
Db 1304 TTTCTCTTGAACCAAAATCCGATCACTGAAAGATTTATTTGGACGCCCAACACCTG 1363
QY 1380 TCAGCCCTTCAGATTCCTCCCTTTTGA 1407
Db 1364 TCAGCCAGTCAAAATTTTCTCCTGGGGA 1391

RESULT 15
HUMP70S6KA 2346 bp mRNA, linear PRI 27-APR-1993
LOCUS Human p70 ribosomal S6 kinase alpha-I
DEFINITION M60724.1 GI:189507
ACCESSION M60724.1
VERSION 1
KEYWORDS p70 ribosomal S6 kinase alpha-I
SOURCE Human liver hepatoma, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2346)
Grove, J. R., Banerjee, P., Balasubramanyam, A., Coffey, P. J.,
Pride, D. J., Avnur, J., and Woodgett, J. R.
Cloning and expression of two human p70 S6 kinase polypeptides
differing only at their amino termini
Mol. Cell. Biol. 11 (11), 5541-5550 (1991)
JOURNAL 9201834
MEDLINE 1922062
PUBMED

FEATURES
source location/Qualifiers
1. 2346
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="hepatoma"
/tissue_type="liver"
28. 1605
/codon_start=1
/product="p70 ribosomal S6 kinase alpha-I"
/protein_id="AA36410.1"
/db_xref="GI:189508"
/translation="MRRRRRDGFYPPAPDRDREADMAVDFIDIDQEDAGSEDEL
EEGGOLNESMDHGAGVPELGMHEKPEFISSESVNRGPEKLRPECFELRLVILGKGY
GKVFQVRKVTGANTGKIFAMKYLKAMTVRNKDKPATAEENILIEEVKHPITVDLIY
AQTGSKLILIEYISGGLPMQLEHREGIFMEDTACFTAEISMAIGHLHQGITTRD
LKPENIMLHGHWKLTDFGLCKESIHDSTVHTCGTIEYAPETILMRSGHNRADV
WSLGLMDMLGVAPETGENRKTIDKLCKLNPPLYTOBARDLKLRNAA
RLGAGGADAGEVOAHPEFRHINWELLAKVPEPKPLQSEEDVSOQSKFTPTQPV
DSDDSTLSEANOVLEFRTYVAIVSLVESEKESFEPEIRSPRRIRSPRPVSVK
FSPDQWKGASASTANPOTPYEPMETSIGIQMDVTNMGESAPLPIQPNSPGPKK
QAPMISKRPEHLRNL"

BASE COUNT 750 a 453 c 358 g 585 t

ORIGIN
Query Match 34.1%; Score 619.8; DB 9; Length 2346;
Best Local Similarity 70.5%; Pred. No. 7.8e-115;
Matches 824; Conservative 0; Mismatches 345; Indels 0; Gaps 0;

QY 240 TGGGACATATGAGAGGTGGAGCTGACTGAGACCAAGCGTGAACGTTGGCCAGACGCA 299
Db 224 TGGACATTTGTGAAATTTGAAATCTCAGAAATCTGATGGAACAGAGGCGCGAAAAA 283
QY 300 TGGGGCCCACTGCTTGGAGCTGCTGCTGTGTGGGCAAGGGGGGCTATGGCAAGTGT 359
Db 284 TCAGACAGAAATTTTGTGACTATCTGGGTACTGTGTAAGGGGCTATGGAAGGTTT 343
QY 360 TCCAGGTGCGAAAGGTGCAAGGCAACCTTGGGCAAAATATATGCAATGAAGTCTTA 419
Db 344 TTCAAGTACGAAAGATTAAGAGAGCAAAATACGTGGAAATATTTGGCATGAAGTCTTA 403
QY 420 GGAAGGCCAAATTTGTGCGCAATGCCAGAGACACACACAGCGGCTGAGCGGAACA 479
Db 404 AAAAGGCAATGATAGTAAAGAAATGCTAAAGATACAGCTCATACAAAAGCAAGCAATA 463
QY 480 TTCTAGATGAGTGAAGCAACCTTTATTTGAGACCTGGGCTTGCCTCCAGACTGTG 539
Db 464 TTCTGGAGCAAGTAAAGCATCCCTTCATCGTGAATTTATTTATGCTTTACAGACTGTG 523
QY 540 GCAAACTCTACCTCATCTTGAAGTGCCTCAGTGGGCGAGCTCTTACAGCATCTGAGC 599
Db 524 GAAACCTCATCTCATCTTGAATCTGATGATCTGAGAGAGAACTATTTATGACACTTGA 583
QY 600 GAGAGGCAATCTTCTGGAAGATACGGCTGCTTCTTACCTGGCTGAGATCAGCTGGCC 659
Db 584 GAGAGGCAATATTTATGGAAGACACTGCGCTTTTACTTGTGAGAAATCTCCATGGCTT 643
QY 660 TGGGCACTCCACCTCCAGACCATCATCTACCGGGGACCGCAAGCAATCATGTC 719
Db 644 TGGGCACTTTACATCAAAAGGATCATCTACAGAGACCTGAAAGCCGAGAAATATATG 703
QY 720 TCAGACGCCAGGGCCACATCAACGACCTTTGGACTCTGCAAGAGTCTATCATC 779
Db 704 TTATATCACAAGGTCAATGTGAATCTTAACAGCTTTGGACTATCAAAAGATCTATTC 763
QY 780 AGGGCGGCTCAGCTCAGCTTCTGGGCACTTTGAGTACATATGAGCCCTGAGATCTG 839
Db 764 ATGAACAGTCAACACACACTTTTGTGGAACATTAATACATGAGCCCTGAAATCTTGA 833
QY 840 TGGCAGTGGCCCAACCGGGCTGTGAGAGTGTGAGAGCTGGGGGCTGATGACGCA 899
Db 824 TGAGAAAGTGGCCCAATCTGCTGTGATTTGGAGTTTGGAGCAATTAATATATGACA 883
QY 900 TGCTCACTGATGCGCGCCCTTTACCGCAGAGAACCGGAAGAAACCATGATTAAGATCA 959
Db 884 TGCTGACTGAGAGCACCCCATTCATCTGGGAGAAATGAAGAAACAAATGACAAATTC 943
QY 960 TCAGGGGCAAGCTGGCAGCTGCCCTTACCTCAGACCCAGATGCGCGGAGCTTGTCAAA 1019
Db 944 TCAATGTAACCTCAATTTGCTCTCTCTACTCAGACAGAGAGCAAGATCTGCTTAAAA 1003
QY 1020 AGTTTCTGAAGAGGAATCCAGCCAGCGGATTTGGGGTGGCCAGGAGTGTGATG 1079
Db 1004 AGTGTGTAAGAAAGAAATGCTGCTTCTGTCTGTGGAGCTGTCTCTGGGAGCGTGGAGAA 1063
QY 1080 TGCAGAGACATCCCTTTTTCGGGACATGAAATTGGGAGACACCTTCTGGCTGCGGTGTG 1139
Db 1064 TTCAAGCTCATTCATCTTATAGACATTAATCTGGGAAGAACTTGTGGCTGAAAGGTGG 1123
QY 1140 ACCGCCCTTCAGAGCCCTGCTCAGTCAAGAGAGAGAGTGAACGATTTGATACCCGCT 1199
Db 1124 AGGCCCTTTTAAACCTCTCTTCAATCTGAAAGAGATGTAATGATTTGATTTCCAAAGT 1183
QY 1200 TCACAGGCGAGCGCGGTGGAGATGCTGATGACACAGCCCTCAGAGAGAGTGCACAC 1259
Db 1184 TTACAGCTCAGACACCTGTGACAGCCAGATGATCACTCACTGAGAAAGTGCACATC 1243

Tue Nov 19 10:45:03 2002

us-09-762-258-1.rge

Page 17

OY	1280	AGGCGCTTCGAGGCTTCACATAGCTAGGCGCGCTCTCTCTGACAGCATCAAGAGAGGCT	1319
Db	1244	AGGCTTTTCGGGTTTTCATATGATGGCTCCATCTGTACTGTAAGTGTGAAAGAAAAGT	1303
OY	1320	TCCTCTTCAGGCCAAGCTGCGGTCAACCCAGGCGCTCAACAGTAGTGGCCCCGGGCTCCCG	1379
Db	1304	TTTTCTTTGGAACCAAAAATCGATCACTCGAAGATTTTATGGCGCCACGAACACTGTG	1363
OY	1380	TCAGCCCCCTCAAGTTCCTCCCTTTTGA	1407
Db	1364	TCAGCCCACTCAAAATTTTCTCTCGGGGA	1391

Search completed: November 18, 2002, 20:20:12
Job time : 3345 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2002, 00:31:27 ; Search time 2062 Seconds
(without alignments)
14263.338 Million cell updates/sec

Title: US-09-762-258-1
Perfect score: 1816
Sequence: 1 gagagagagagagagagaga.....aaaaaaaaaaaaaaaaaa 1816

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estnu: *
5: em_estcov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rod: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1183.6	65.2	1834	11	AK014412 Mus muscu
2	964.4	53.1	992	9	AL529444 AL529444
3	897.6	49.4	1037	14	B0059474 AGENCOURT
4	890.2	49.0	1076	14	BM923000 AGENCOURT
5	886.8	48.8	932	9	AL519475 AL519475
6	868.4	47.8	1005	13	BM423942 AGENCOURT

7	859.6	47.3	943	14	B0643418
8	856.8	47.2	1014	14	B0052654
9	844.2	46.5	849	9	AL527983
10	842	46.4	949	14	B0642404
11	840.4	46.3	895	9	AL521570
12	837.4	46.1	907	9	AL563023
13	836.2	46.0	952	14	B0918927
14	827.4	45.6	1075	14	B0062171
15	806.2	44.4	1048	14	B0052262
16	802	44.2	1018	14	B0057747
17	797	43.9	1049	14	B0054269
18	795.2	43.8	850	9	AL560524
19	794.2	43.7	1080	14	B0062488
20	792.2	43.6	834	12	BE792760
21	785	43.2	913	9	AL563439
22	778.6	42.9	1176	14	B0061526
23	776.4	42.8	1044	14	B0072582
24	773.6	42.6	865	12	BE792968
25	765.8	42.2	793	13	B1907389
26	762.4	42.0	764	12	BG773589
27	762	42.0	789	9	AL525066
28	760.6	41.9	854	14	B0431606
29	755.8	41.6	883	14	B0877063
30	755.4	41.6	757	13	B1084346
31	754.8	41.6	867	13	B1821158
32	754.2	41.5	767	9	AL519476
33	753.8	41.5	997	14	B0948653
34	751.4	41.4	891	12	BG829030
35	743	40.9	858	14	B0961675
36	742.4	40.9	923	14	B0890823
37	739.2	40.7	783	13	B1825778
38	738.2	40.6	1109	14	B0058742
39	736.8	40.6	814	12	BG488888
40	731.4	40.3	946	9	AL562007
41	726	40.0	757	13	BM020218
42	719.8	39.6	1082	13	BM561338
43	711.4	39.2	946	14	B0668937
44	709.6	39.1	1036	12	BE882270
45	707.2	38.9	780	13	B1224008

ALIGNMENTS

RESULT 1
AK014412
LOCUS 1834 bp mRNA linear HTC 19-JAN-2002
DEFINITION Mus musculus 18 days pregnant adult female placenta and extra embryonic tissue cDNA, RIKEN full-length enriched library, clone:3830402N06; protein tyrosine phosphatase, receptor type, C polypeptide-associated protein, full insert sequence.
ACCESSION AK014412
VERSION AK014412.1 GI:12852247
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) 18 days pregnant adult female placenta and extra embryonic tissue cDNA to mRNA, clone:11b-RIKEN full-length enriched mouse cDNA library clone:3830402N06.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itch, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374

Db 361 ACACACAGGGGCTGAGCGGAACATCTTAGAGTCAGTTAAAGCACCCCTTTATTGTGGAAGT 420
QY 517 GGCCTATGCTTTCACAGATGTTGGCAAACTCTACCTCATCTTGTAGTGGCTCAGTGGTG 576
Db 421 GGGCTATGCTTTCACAGATGTTGGCAAACTCTACCTCATCTTGTAGTGGCTCAGTGGTG 480
QY 577 CGAGCTCTTCACAGATGTTGGCAAACTCTTCTGGAAGATPACGGCTGCTTCTA 636
Db 481 CGAGCTCTTCACAGATGTTGGCAAACTCTTCTGGAAGATPACGGCTGCTTCTA 540
QY 637 CCGGCTGAGATGATGCTGGCCCTGGGCGCATCTCCACTCCAGGCGATCATCTACCGGGA 636
Db 541 CCGGCTGAGATGATGCTGGCCCTGGGCGCATCTCCACTCCAGGCGATCATCTACCGGGA 600
QY 697 CCTCAAGCCCGAGAACATCATCTGCTCAGACGCCAGGCCCATCAACTGACGACTTTGG 756
Db 601 CCTCAAGCCCGAGAACATCATCTGCTCAGACGCCAGGCCCATCAACTGACGACTTTGG 660
QY 757 ACTCTGCAAGAGATCTATCCATGAGGGCGCGTCACTCAGACCTTCTGGCGACATTTGA 816
Db 661 ACTCTGCAAGAGATCTATCCATGAGGGCGCGTCACTCAGACCTTCTGGCGACATTTGA 720
QY 817 GTACATAGCCCTTGTAGATTTGTGGCGCATGTCGCGCCCTTTACCGCAGAGAACG 876
Db 721 GTACATAGCCCTTGTAGATTTGTGGCGCATGTCGCGCCCTTTACCGCAGAGAACG 780
QY 877 CCGGCGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 936
Db 781 CCGGCGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 937 GAAGAAACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 996
Db 841 GAAGAAACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
QY 997 AGATGCGCCGGGACTGTCTCAAAAGTTTCTGAACCGGAACCGACGAGGATTTGGGG 1056
Db 901 AGATGCGCCGGGACTGTCTCAAAAGTTTCTGAACCGGAACCGACGAGGATTTGGGG 960
QY 1057 TGCGCCAGGAGGATGCTGCTGATGT 1080
Db 961 GTGGCCAGGAGGATGCTGCTGATGT 984

RESULT 3
LOCUS BQ059474 1037 bp mRNA linear EST 29-MAR-2002
DEFINITION AGEMOUNT 7050085 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5815533
ACCESSION BQ059474
VERSION BQ059474.1 GI:19818814
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1037)
AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CM2070 row: 0 column: 22
High quality sequence stop: 611.
Location/Qualifiers
1..1037

FEATURES
source
1..1037
/organism="Homo sapiens"

/db_xref="taxon:9606"
/clone="IMAGE:5815533"
/clone_lib="NIH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: This is a NIH-MGC
Library."

BASE COUNT 206 a 356 c 282 g 191 t 2 others
ORIGIN

Query Match 49.4%; Score 897.6; DB 14; Length 1037;
Best Local Similarity 95.4%; Pred. No. 1.7e-140;
Matches 990; Conservative 0; Mismatches 36; Indels 12; Gaps 6;

QY 612 TCCTGAGATGAGGCTGCTGCTTACCTGAGATGATGATGATGATGATGATGATGATGATG 671
Db 1 TCCTGAGATGAGGCTGCTGCTTACCTGAGATGATGATGATGATGATGATGATGATGATG 60
QY 672 ACTCCAGGCGCATCATCTACCGGAGCTCAAGCCGAGAACATCATGCTCAGACGACAG 731
Db 61 ACTCCAGGCGCATCATCTACCGGAGCTCAAGCCGAGAACATCATGCTCAGACGACAG 120
QY 732 GCCACATCAATGACCGGACTTTGGACTGCAAGAGATCTATCCATGAGGGCGGCTCA 791
Db 121 GCCACATCAATGACCGGACTTTGGACTGCAAGAGATCTATCCATGAGGGCGGCTCA 180
QY 792 CTCACACTTCTGCGGACCATGATGATGATGATGATGATGATGATGATGATGATGATG 851
Db 181 CTCACACTTCTGCGGACCATGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 852 ACAACGGGCTGTGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCT 911
Db 241 ACAACGGGCTGTGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCT 300
QY 912 CGCGGCGCTTTACCGAGAGAACCGGAGAAACCATGATGATGATGATGATGATGATG 971
Db 301 CGCGGCGCTTTACCGAGAGAACCGGAGAAACCATGATGATGATGATGATGATGATG 360
QY 972 TGCGACTGCGCCCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATG 1031
Db 361 TGCGACTGCGCCCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 1032 GGAATCCACAGCGGAGATTTGGGTTGGCCAGGAGATGCTGATGTCAGAGACATC 1091
Db 421 GGAATCCACAGCGGAGATTTGGGTTGGCCAGGAGATGCTGATGTCAGAGACATC 480
QY 1092 CTTTTTTCGGGCAATGATTTGGAGAGCTTCTGCGGCTGGGCTGGGCTGGGCTTTCA 1151
Db 481 CTTTTTTCGGGCAATGATTTGGAGAGCTTCTGCGGCTGGGCTGGGCTGGGCTTTCA 540
QY 1152 GGCCTGTGTGACAG 1211
Db 541 GGCCTGTGTGACAG 600
QY 1212 CGCGGCTGAGACGCTGATGACACAGCCCTCAGGAGAGTGCACACAGGCTTCTGG 1271
Db 601 CGCGGCTGAGACGCTGATGACACAGCCCTCAGGAGAGTGCACACAGGCTTCTGG 660
QY 1272 GCTTACATATGAGGGGCGCTGTCTGAGACGATCAAGAGAGGCTTCTCTCTCAG 1331
Db 661 GCTTACATATGAGGGGCGCTGTCTGAGACGATCAAGAGAGGCTTCTCTCTCAG 720
QY 1332 CCAAGCTGCGCTCACCAGGCGGCTCAACAGTATGAGCCCGGAGGCTTCTCTCTCAG 1391
Db 721 CCAAGCTGCGCTCACCAGGCGGCTCAACAGTATGAGCCCGGAGGCTTCTCTCTCAG 780

QY	1392	AGTCCTCCCTTTGAGGGGGTTTGCGCCACGCCACCGCTCCGGAGCCACAGAGCTAC	1451
Db	761	AGTTCTCCCTTTTGAGGGGGTTTGCGCCACGCCACCGCTCCGGAGCCACAGAGCTAC	840
QY	1452	CTCTACCTCCACCTCTGCGCACCGCGCCCTCGAGCACCGCCCTTCCCATCCGTC	1511
Db	841	CTCTACCT-CACTCTCTGCCA-CGGGCGCGCTCTCGACACACGCCCTTCTCCATCGTC	898
QY	1512	CCCCCTC-AGGGACACAGAGCTCCAAAG-AGGGCCGTGGGGCTCCAGGGCCCTAGGAAGC	1569
Db	899	CCCCCTCAAGGAGACCAAGAGTCACAAAGAGGGAGCCNGGGGCTTACAGGGCCCTAGGAAGC	958
QY	1570	CGGGGGGGGGGTGAGGGTG-----CCCTTGAGCCCTTCCCTCGCGCTGTGAGAGC--A	1621
Db	959	CCCTTTTGGGGGGGTAAAGGTACCCCTTGACCCCTGACCCCTGGCGGTTGTAAACCA	1018
QY	1622	GCAGGACCTGGGCCAGT	1639
Db	1019	CCGGACCTTGGGCCAGT	1036
RESULT 4			
LOCUS	BM923000	1076 bp	mRNA linear EST 12-MAR-2002
DEFINITION	AGNCOURT_6632221 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5756950		
ACCESSION	BM923000		
VERSION	BM923000.1 GI:19373379		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	NIH-MGC http://mgc.ncl.nih.gov/		
JOURNAL	1 (bases 1 to 1076)		
COMMENT	Unpublished (1999)		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: Life Technologies, Inc.		
	cDNA Library Preparation: Life Technologies, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.lnl.gov		
	Plate: L1AM12798 row: f column: 23		
	High quality sequence stop: 670.		
FEATURES			
source	location/Qualifiers		
	1..1076		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:5756950"		
	/clone_11b="NIH_MGC_118"		
	/tissue_type="Leukocyte"		
	/lab_host="DH10B"		
	/note="Vector: pCMV-SPORT6; site.1: NotI; site.2: EcoRV		
	(destroyed); RNA source: Leukocytes from anonymous pool of		
	non-activated adult donors. Library is oligo-dT primed		
	and directionally cloned (EcoRV site is destroyed upon		
	cloning). Average insert size 1.7 kb, insert size range		
	1.2-3.3 kb. Library is normalized and enriched for		
	full-length clones and was constructed by C. Gruber		
	(Invitrogen). Research Genetics tracking code 027. Note:		
	this is a NIH_MGC Library."		
BASE COUNT	229 a 313 c 333 g 198 t	3 others	
ORIGIN			
Query Match	49.0%:	Score 890.2:	DB 14:
Best Local Similarity	96.9%:	Pred. No.2.9e-139:	Length 1076:
Matches 949:	Conservative 0:	Mismatches 25:	Indels 5:
			Gaps 4:
QY	86	GGCCACAGGGCCCGGGGGCCGGCCCGCCAGTGGCGGGCGCTGTGATTTGATTTGGATTGGAG	145

[illegible]

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library "

Query Match 47.8%; Score 868.4; DB 13; Length 1005;

Best Local Similarity 98.3%; Pred. No. 1.3e-135; Matches 899; Conservative 0; Mismatches 12; Indels 4; Gaps 2;

BASE COUNT 218 a 288 c 320 g 177 t 2 others
 ORIGIN
 Query Match 47.8%; Score 868.4; DB 13; Length 1005;
 Best Local Similarity 98.3%; Pred. No. 1.3e-135;
 Matches 899; Conservative 0; Mismatches 12; Indels 4; Gaps 2;
 QY 86 GGCCGACGGCCCGGGGGCCGCCATGGCGCCGTTGATTGGATTGGAG 145
 DB 1 GGCCGACGGCCCGGGGGCCGCCATGGCGCCGTTGATTGGATTGGAG 60
 QY 146 ACGGAGGAAGCAGAGAGGGGAGGGCCAGCAGACCTACCCCGGGAGCATGTCC 205
 DB 61 ACGGAGGAAGCAGAGAGGGGAGGGCCAGCAGACCTACCCCGGGAGCATGTCC 120
 QY 206 CTTGCGGAGTTGAGGGCAGCTGGCCTAGAGCCTGTGGACACTATGAAGAGTGGAGCTG 265
 DB 121 CTTGCGGAGTTGAGGGCAGCTGGCCTAGAGCCTGTGGACACTATGAAGAGTGGAGCTG 180
 QY 266 ACTGAGACCAAGCTGACGTTGGCCAGAGCGCATGGGCCCCACTGCTTTGAGCTGCTG 325
 DB 181 ACTGAGACCAAGCTGACGTTGGCCAGAGCGCATGGGCCCCACTGCTTTGAGCTGCTG 240
 QY 326 CGTGCTGGGCGAAGGGGGGCTATGGCAAGGTTCAGAGTGGCAAGGTGCAGACGCCACC 385
 DB 241 CGTGCTGGGCGAAGGGGGGCTATGGCAAGGTTCAGAGTGGCAAGGTGCAGACGCCACC 300
 QY 386 AACTTGGGCAAAATATATGCCATGAAAGTCTTAAGGAAGGCCAAATTTGTGGCAATGCC 445
 DB 301 AACTTGGGCAAAATATATGCCATGAAAGTCTTAAGGAAGGCCAAATTTGTGGCAATGCC 360
 QY 446 AAGGACACAGACACACAGGGGCTGAGCGGAACATTCTAGAGTCAAGACACCCCTTT 505
 DB 361 AAGGACACAGACACACAGGGGCTGAGCGGAACATTCTAGAGTCAAGACACCCCTTT 420
 QY 506 ATTGGGAACATGGGCTATGGCTTCAGACTGGTGGCAACCTACCTACCTGAGAGTC 565
 DB 421 ATTGGGAACATGGGCTATGGCTTCAGACTGGTGGCAACCTACCTACCTGAGAGTC 480
 QY 566 CTCAGTGGGCGAGCTTTCACGCATCTGAGCAGAGAGGCGCATCTCTGGAAAGATACG 625
 DB 481 CTCAGTGGGCGAGCTTTCACGCATCTGAGCAGAGAGGCGCATCTCTGGAAAGATACG 540
 QY 626 GCTGCTTCTACCTGGCTGAGATCACGCTGGGCGCATCTCCACCTCCAGGGCATC 685
 DB 541 GCTGCTTCTACCTGGCTGAGATCACGCTGGGCGCATCTCCACCTCCAGGGCATC 600
 QY 686 ATCTACCGGGGACCTCAACCCGAGAACTCATCTCAGCAGCAGAGGCGCATCAACTG 745
 DB 601 ATCTACCGGGGACCTCAACCCGAGAACTCATCTCAGCAGCAGAGGCGCATCAACTG 660
 QY 746 ACCGACTTTGAGCTTGCAGAGAGTCTATCCATGAGGGCGCGTCACTACACCTTTGCG 805
 DB 661 ACCGACTTTGAGCTTGCAGAGAGTCTATCCATGAGGGCGCGTCACTACACCTTTGCG 720
 QY 806 GGCACCATTTGAGTACATGGCCCTGAGATTCTGTGGCAGTGGCCACACCGGGCTGTG 865
 DB 721 GGCACCATTTGAGTACATGGCCCTGAGATTCTGTGGCAGTGGCCACACCGGGCTGTG 780
 QY 866 GACTGGTGGAGGCTGGG-GGGCGCTGATGACACATGCTCATGATGGCGCCCTTAC 924
 DB 781 GACTGGTGGAGGCTGGGCGGCGCTGATGACACATGCTCATGATGGCGCCCTTCA 840
 QY 925 CGCAGAGAACCGGAAGAAACCATGATTAAGTCACTACGAGGCAAGCT---GGCACTGCC 981
 DB 841 CGCAGAGAACCGGAAGAAACCATGATTAAGTCACTACGAGGCAAGCTGGGAGTGGCC 900
 QY 982 CCCCTACTCAACCC 996
 DB 901 CCCCTACTCAACCC 915

RESULT 7
 B0643418 943 bp mRNA linear EST 15-JUL-2002
 LOCUS
 DEFINITION
 AGENCOURT_8485261 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:6305404
 5', mRNA sequence.
 B0643418
 VERSION
 B0643418.1 GI:21767590
 KEYWORDS
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 943)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: rgs@bld-remail.nih.gov
 Tissue Procurement: Lou Staudt
 cDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
 http://image.lnl.gov
 plate: LCM2527 row: k column: 05
 High quality sequence stop: 775.
 Location/Qualifiers
 1. 943
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6305404"
 /clone_id="NIH_MGC_99"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lymph. Vector: POT87. Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCCGAGG(6). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

FEATURES

source

BASE COUNT 200 a 275 c 298 g 169 t 1 others
 ORIGIN

Query Match 47.3%; Score 859.6; DB 14; Length 943;
 Best Local Similarity 97.7%; Pred. No. 3.9e-134;
 Matches 893; Conservative 0; Mismatches 19; Indels 2; Gaps 2;

QY 86 GGCCGACGGCCCGGGGGCCGCCATGGCGCCGTTGATTGGATTGGAG 145
 DB 28 GGCCGACGGCCCGGGGGCCGCCATGGCGCCGTTGATTGGATTGGAG 87
 QY 146 ACGGAGGAAGCAGAGAGGGGAGGGCCAGCAGACCTACCCCGGGAGCATGTCC 205
 DB 88 ACGGAGGAAGCAGAGAGGGGAGGGCCAGCAGACCTACCCCGGGAGCATGTCC 147
 QY 206 CTTGCGGAGTTGAGGGCAGCTGGCCTAGAGCCTGGGACACTATGAAGAGTGGAGCTG 265
 DB 148 CTTGCGGAGTTGAGGGCAGCTGGCCTAGAGCCTGGGACACTATGAAGAGTGGAGCTG 207
 QY 266 ACTGAGACCAAGCTGACGTTGGCCAGAGCGCATGGGCCCCCACTGCTTTGAGCTGCTG 325
 DB 208 ACTGAGACCAAGCTGACGTTGGCCAGAGCGCATGGGCCCCCACTGCTTTGAGCTGCTG 267
 QY 326 CGTGCTGGGCGAAGGGGGCTATGGCAAGGTTCAGAGTGGCAAGAGTGCAGAGCAC 385
 DB 268 CGTGCTGGGCGAAGGGGGCTATGGCAAGGTTCAGAGTGGCAAGAGTGCAGAGCAC 327

QY 386 AACTTGGGCAAAATATATGTCATGAAAGTCTTAAGGAGGCCAAAATTGTGGCAATGCC 445
 DB 328 AACTTGGGCAAAATATATGTCATGAAAGTCTTAAGGAGGCCAAAATTGTGGCAATGCC 387
 QY 446 AAGGACACAGCACACACAGGCGGTGAGCGGAACATTTAGAGTCAGTGAAGCAACCCCTTT 505
 DB 388 AAGGACACAGCACACACAGGCGGTGAGCGGAACATTTAGAGTCAGTGAAGCAACCCCTTT 447
 QY 506 ATTGTGAAGTGGCGATATGCTTTCAGACTGTGTGGCAAACTTACCTCATCTTGTGATGC 565
 DB 448 ATTGTGAAGTGGCGATATGCTTTCAGACTGTGTGGCAAACTTACCTCATCTTGTGATGC 507
 QY 566 CTCAGAGTGGCGGACGCTTTCAGACTGTGTGGCAAACTTACCTCATCTTGTGATGC 625
 DB 508 CTCAGAGTGGCGGACGCTTTCAGACTGTGTGGCAAACTTACCTCATCTTGTGATGC 567
 QY 626 GCTGTCTTACCTGCTGATCAGCTGTGTGGCAAACTTACCTCATCTTGTGATGC 685
 DB 568 GCTGTCTTACCTGCTGATCAGCTGTGTGGCAAACTTACCTCATCTTGTGATGC 627
 QY 686 ATCTACCGGGACCTCAAGCCGAGAACATCATCTCAGCAGCGGCGCCATCAAACTG 745
 DB 628 ATCTACCGGGACCTCAAGCCGAGAACATCATCTCAGCAGCGGCGCCATCAAACTG 687
 QY 746 ACCGACTTTGAGACTCTGCAAGAGTCTATCATGAGGCGCGCTCACTACACCTTCTGC 805
 DB 688 ACCGACTTTGAGACTCTGCAAGAGTCTATCATGAGGCGCGCTCACTACACCTTCTGC 747
 QY 806 GGCACCATTTGAGACTCTGCAAGAGTCTATCATGAGGCGCGCTCACTACACCTTCTGC 865
 DB 748 GGCACCATTTGAGACTCTGCAAGAGTCTATCATGAGGCGCGCTCACTACACCTTCTGC 807
 QY 866 GACTGTGAGAGCTGTGGGGGCTGTATGATGACATGCTCAGTGTGAGGCGCGCTTCA-C 924
 DB 808 GACTGTGAGAGCTGTGGGGGCTGTATGATGACATGCTCAGTGTGAGGCGCGCTTCA-C 867
 QY 925 CGGAGAGAACCGGAGAAAACCATGG-ATTAAGTCAATCAGGGGCAAGCTGGCACTGCCCC 983
 DB 868 CGGAGAGAACCGGAGAAAACCATGG-ATTAAGTCAATCAGGGGCAAGCTGGCACTGCCCC 927
 QY 984 CTAACCTCAACCCCA 997
 DB 928 CCCCCCTTACTCA 941
 RESULT 8
 LOCUS BQ052654 1014 bp mRNA linear EST 29-MAR-2002
 DEFINITION AGENCOURT_6871884 NIH_MGC_106 Homo sapiens CDNA clone IMAGE:5934028
 5', mRNA sequence.
 ACCESSION BQ052654
 VERSION BQ052654.1 GI:19811994
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 1014)
 NIH-MGC <http://mhc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Dr. Daniel McVeyar
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LICM2119 row: 1 column: 05
 High quality sequence stop: 703.
 Location/Qualifiers

source 1. 1014
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5934028"
 /clone_1lb="NIH_MGC_106"
 /tissue_type="natural killer cells, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; CDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."
 BASE COUNT 225 a 312 c 278 g 197 t 2 others
 ORIGIN
 Query Match 47.2%; Score 856.8; DB 14; Length 1014;
 Best Local Similarity 98.4%; Pred. No. 1,1e-133;
 Matches 897; Conservative 0; Mismatches 12; Indels 3; Gaps 3;
 QY 356 GTGTTCCAGGTGGGAAAGGTCGAAGGACCAACTT-GGGCAAAATATATGTCATGAACT 414
 DB 1 GTGTTCCAGGTGGGAAAGGTCGAAGGACCAACTTGGGCAAAATATATGTCATGAACT 60
 QY 415 CCTTAAGGAAGGCCAAATTTGTGGCAATGCCAAGGACACAGCACACACAGGCGTGAAGC 474
 DB 61 CCTTAAGGAAGGCCAAATTTGTGGCAATGCCAAGGACACAGCACACACAGGCGTGAAGC 120
 QY 475 GAACATTTAGAGTCAAGTGAAGACCCCTTATTTGTGAAGTGGCTTATGCTTCCAGAC 534
 DB 121 GAACATTTAGAGTCAAGTGAAGACCCCTTATTTGTGAAGTGGCTTATGCTTCCAGAC 180
 QY 535 TGGTGGCAAACTTACCTCATCTTGTAGTGGCTCATGTGGGAGGAGCTTTCACGACAT 594
 DB 181 TGGTGGCAAACTTACCTCATCTTGTAGTGGCTCATGTGGGAGGAGCTTTCACGACAT 240
 QY 595 GGAGCGAGAGGGGCAATCTTCTGGAAGATAGCGGCTCTTCTCACTGCTGAGTACAGCT 654
 DB 241 GGAGCGAGAGGGGCAATCTTCTGGAAGATAGCGGCTCTTCTCACTGCTGAGTACAGCT 300
 QY 655 GGCCCTGGGCAATCTTCACTCCAGGGCATCATCTACCGGAGCTTAACCCGAGAACT 714
 DB 301 GGCCCTGGGCAATCTTCACTCCAGGGCATCATCTACCGGAGCTTAACCCGAGAACT 360
 QY 715 CATGCTCAGAGGACGAGGCGCACATCAACCTGACCCGACTTTGGACTGCAAGAGCTAT 774
 DB 361 CATGCTCAGAGGACGAGGCGCACATCAACCTGACCCGACTTTGGACTGCAAGAGCTAT 420
 QY 775 CCATGAGGGGCGGCTACACACCTTTCGCGGACACATTAAGTACATGAGTGGCCCTGAGAT 834
 DB 421 CCATGAGGGGCGGCTACACACCTTTCGCGGACACATTAAGTACATGAGTGGCCCTGAGAT 480
 QY 835 TCTGTGGCGCATGGGCAACACCGGCTGTGACTGTGTGGAGCTTGGGGCCCTGATGTA 894
 DB 481 TCTGTGGCGCATGGGCAACACCGGCTGTGACTGTGTGGAGCTTGGGGCCCTGATGTA 540
 QY 895 CGACATGCTCAGTGGATGCGCGGCTTTACCGGAGAGAACCGGAAACCATGATGA 954
 DB 541 CGACATGCTCAGTGGATGCGCGGCTTTACCGGAGAGAACCGGAAACCATGATGA 600
 QY 955 GATCATCAGGGGCAAGCTGGCACTGCCCCCTTACCTCAACCCAGATGAGTGGCGGACCTTGT 1014
 DB 601 GATCATCAGGGGCAAGCTGGCACTGCCCCCTTACCTCAACCCAGATGAGTGGCGGACCTTGT 660
 QY 1015 CAAAAAGTTTCTGAAGGAAATCCAGCCAGCGGATTTGGGGTGGCCAGGGGATGCTCC 1074
 DB 661 CAAAAAGTTTCTGAAGGAAATCCAGCCAGCGGATTTGGGGTGGCCAGGGGATGCTCC 720
 QY 1075 TGATGTGAGAGACATCCCTTTTCCGAGACATGAATTTGGAGAGCACTTGGCCCTGGGG 1134
 DB 721 TGATGTGAGAGACATCCCTTTTCCGAGACATGAATTTGGAGAGCACTTGGCCCTGGGG 780

QY	1135	TGTGACCCCTTTTCAGGCGCCCTGCTCAGTCACAGGAGGACGTCAGGACCTTTGATAC	1194
Db	761	TGTGACCCCTTTTCAGGCGCCCTGCTCAGTCACAGGAGGACGTCAGGACCTTTGATAC	840
QY	1195	CCGCTTTCACAGGCGGACGCGCGGT-GGACAGTCTGTATGACACAG-CCCTACGAGAGT	1252
Db	841	CCGCTTTCACAGGCGGACGCGCGGTGAGACAGTCTGTATGACACAGCCCTTACAGAGAGT	900
QY	1253	GCCACACGAGCC 1264	
Db	901	GCCACACGAGCC 912	
RESULT 9			
LOCUS	AL527983	849 bp	MRNA
DEFINITION	AL527983 LTR_NFL003.NBC3	Homo sapiens	CDNA clone CS0DC027YH21 5
ACCESSION	AL527983		prime, mRNA sequence.
VERSION	AL527983.1	GI:12791476	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Li, W. B., Gruber, C., Jessee, J. and Polayes, D.		
JOURNAL	Full-length cDNA libraries and normalization		
COMMENT	Unpublished (2001)		
FEATURES	Genoscope - Centre National de Sequencage		
Source	BP 191 91006 EVRY cedex - France		
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.		
	Location/Qualifiers		
	1..849		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="CS0DC027YH21"		
	/clone_lib="LTR_NFL003_NBC3"		
	/sex="male"		
	/issue_type="neuroblastoma cells"		
	/lab_host="DH10B"		
	/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA		
	was primed with a NotI-oligo(dT) primer. Five prime end		
	enriched, double-stranded cDNA was digested with NotI and		
	cloned into the NotI and EcoRV sites of the pCMVSPORT 6		
	vector. Library was normalized. Library was constructed		
	by Life Technologies. Contact : Feng Liang Life		
	Technologies, a division of Invitrogen 9800 Medical Center		
	Drye Rockville, Maryland 20850, USA Fax : (1) 301 610		
	8371 Email : fliang@lifetech.com URL :		
	http://fulllength.invitrogen.com"		
BASE COUNT	178 a	242 c	268 g
ORIGIN		159 t	2 others
Query Match	46.5%;	Score 844.2;	DB 9; Length 849;
Best Local Similarity	99.8%;	Pred. No. 1.5e-131;	
Matches 843;	Conservative	2; Mismatches	0; Indels
			0; Gaps
			0;
QY	86	GCCGACGAGGCGCCGCGGCGCGCGCCGATGCGCGCTGTGATTTGGATTGGAG	145
Db	5	GCCGACGAGGCGCCGCGGCGCGCGCCGATGCGCGCTGTGATTTGGATTGGAG	64
QY	146	ACGAGGAAAGCGAGGCGAGGCGAGGCGAGCGATGACGCCCGCGGACGATGTC	205
Db	65	ACGAGGAAAGCGAGGCGAGGCGAGGCGAGCGATGACGCCCGCGGACGATGTC	124
QY	206	CTTGCCGAGTTGAGGCGAGCTGCTTAGAGCCTGTGGAGACACTATGAGAGGTGAGCTG	265
Db	125	CTTGCCGAGTTGAGGCGAGCTGCTTAGAGCCTGTGGAGACACTATGAGAGGTGAGCTG	184
QY	266	ACTGACACGAGCTGATGCTTGGCCAGAGGCGATCGGCCCCACACTGTTGAGCTGCTG	325

Db	185	ACTGAGACCGGTACAGTGTGGCCACAGGCGATCGGGCCCACTGCTTTGAGCTGTG	244
QY	328	CGTGTCTGGGCGAAGGGGGCTATGGCAAGTGTTCACAGTTCGGAAGGTGCAGAGGCAC	385
Db	245	CGTGTCTGGGCGAAGGGGGCTATGGCAAGGTGTTCACAGTTCGGAAGGTGCAGAGGCAC	304
QY	386	AACCTTGGGCAAAATATATGGCCATGGAAATCTCAAGGAAGGCCAAATTTGTGCGCAATGCC	445
Db	305	AACCTTGGGCAAAATATATGGCCATGGAAATCTCAAGGAAGGCCAAATTTGTGCGCAATGCC	364
QY	446	AAGGACACAGCACACACACAGGGCTAGCGGAACATTTCTAGAGTCAAGTCAACACCCCTTT	505
Db	365	AAGGACACAGCACACACACAGGGCTAGCGGAACATTTCTAGAGTCAAGTCAACACCCCTTT	424
QY	506	ATTGTGGAACCTGGCCCTATGCCCTTCCAGACTGGTGGCAAACTCTACCTCATCTTGAATGC	565
Db	425	ATTGTGGAACCTGGCCCTATGCCCTTCCAGACTGGTGGCAAACTCTACCTCATCTTGAATGC	484
QY	566	CTCATGTGGTGGGAGACTCTTTCACGATCTGGAGGACGACAGAGGGCATTTCTTGGAGATACG	625
Db	485	CTCATGTGGTGGGAGACTCTTTCACGATCTGGAGGACGACAGAGGGCATTTCTTGGAGATACG	544
QY	626	GCCTGCTTCTACCTGGCTGAGATCAACGGTGGCCCTGGGGCATCTTCACCTCCAGGGCATC	685
Db	545	GCCTGCTTCTACCTGGCTGAGATCAACGGTGGCCCTGGGGCATCTTCACCTCCAGGGCATC	604
QY	686	ATCTACCGGGACCTCAAGCCCGAGAAACATCATGCTCTCAGACAGCCAGGGCCACATCAACTG	745
Db	605	ATCTACCGGGACCTCAAGCCCGAGAAACATCATGCTCTCAGACAGCCAGGGCCACATCAACTG	664
QY	746	ACCGACTTTGGACTCTGCAGAGAGTCTATCCATGAGGGCCCGGTACTCACACCTTTGCG	805
Db	665	ACCGACTTTGGACTCTGCAGAGAGTCTATCCATGAGGGCCCGGTACTCACACCTTTGCG	724
QY	806	GGCACCATTTGATACATGAGCCCTCAGATTTCTGGAGGCGAGAGGGCCACACCGGGCTGTG	865
Db	725	GGCACCATTTGATACATGAGCCCTCAGATTTCTGGAGGCGAGAGGGCCACACCGGGCTGTG	784
QY	866	GACTGTGGAGAGCTGGGGCCCTGATGTACAGACATGCTCACATGATCGCCGCCCTTTTACC	925
Db	785	GACTGTGGAGAGCTGGGGCCCTGATGTACAGACATGCTCACATGATCGCCGCCCTTTTACC	844
QY	926	GCAGA 930	
Db	845	GCAGA 849	
RESULT 10			
LOCUS	B0642404	949 bp	linear EST 15-JUL-2002
DEFINITION	AGENCOURT_8485437 NIH_MGC_99 Homo sapiens cdna clone IMAGE:6305367		
ACCESSION	B0642404		
VERSION	B0642404.1	GI:21766576	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 949)		
JOURNAL	NIH-MGC http://mhc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strusberg, Ph.D.		
	Email: cgabs-remail.nih.gov		
	Tissue Procurement: Lou Staudt		
	cDNA Library Preparation: Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.llnl.gov		

QY 1591 CTTGACCCCTGTCCTCGCGGCTGTGAGACAGACACCCTGGGCCAGTTCCAGAGACCT 1650
|||||
Db 129 CTTGACCCCTGTCCTCGCGGCTGTGAGACAGACACCCTGGGCCAGTTCCAGAGACCT 70
|||||
QY 1651 GGGGGTGTGCTGCGGGGTGGGTGTGAGTGCATGAAGTGTGCTGCTGCGTGGGGCAGC 1710
|||||
Db 69 GGGGGTGTGCTGCGGGGTGGGTGTGAGTGCATGAAGTGTGCTGCTGCGTGGGGCAGC 10
|||||
QY 1711 TGTGCCCCCT 1719
|||||
Db 9 TGTGCCCCCT 1
|||||
RESULT 13
BQ918927 952 bp mRNA linear EST 20-AUG-2002
LOCUS AGENCOURT 8772806 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6372043
DEFINITION 5', mRNA sequence.
ACCESSION BQ918927
VERSION BQ918927.1 GI:22333625
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.mc.man.ac.uk/1 (bases 1 to 952)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1CM2547 row: c column: 20
High quality sequence stop: 648.
Location/Qualifiers
1. 952
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6372043"
/clone_1lb="NIH_MGC_18"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC library."

BASE COUNT 206 a 275 c 293 g 174 t 4 others
ORIGIN
Query Match 46.0%; Score 836.2; DB 14: Length 952;
Best Local Similarity 96.7%; Pred. No. 3.1e-130;
Matches 897; Conservative 0; Mismatches 24; Indels 7; Gaps 4;

QY 87 GCGAGCGGCGCGCGCGCGCGCGCGCGCATGCGCGCGCTGTGATTGATTGGATTGGAGA 146
|||||
Db 1 GCGGAGGGGCGCGCGCGCGCGCGCGCGCATGCGCGCGCTGTGATTGATTGGATTGGAGA 60
|||||
QY 147 CGGAGAGGCGAGCGAGCGGCGAGCGGCGAGCGCTCAAGCCCGCGAGCGATGTCCCG 206
|||||
Db 61 CGGAGAGGCGAGCGAGCGGCGAGCGGCGAGCGAGCGCTCAAGCCCGCGAGCGATGTCCCG 120
|||||
QY 207 TTGCCAGTTGAGGGGAGCTGGCTGAGAGCTGTGGAGACATGTGAAGAGTGGAGCTGA 266
|||||

Db 121 TTGCCAGTTGAGGGGAGCTGGCTGAGAGCTGTGTGGACATGTGAAGAGTGGAGCTGA 180
|||||
QY 267 CTTGAGACAGCGTGAACGTTTGGCCAGAGCGCATCGGGCCCACTGCTTTGAGCTGTGC 326
|||||
Db 181 CTGAGACAGCGTGAACGTTTGGCCAGAGCGCATCGGGCCCACTGCTTTGAGCTGTGC 240
|||||
QY 327 GTGTGCTGGGCAAGGGGGCTATGGCAAGTGTTCAGTGGCAAGTGTGCAAGGACCA 386
|||||
Db 241 GTGTGCTGGGCAAGGGGGCTATGGCAAGTGTTCAGTGGCAAGTGTGCAAGGACCA 300
|||||
QY 387 ACTTGGGCAAAATATATGCGATGAAGTCTTAAGGAAGGCCAAATATGGCAATGCCA 446
|||||
Db 301 ACTTGGGCAAAATATATGCGATGAAGTCTTAAGGAAGGCCAAATATGGCAATGCCA 360
|||||
QY 447 AGGACACAGCACACACAGCGGCTGAGCGGAGCAATCTTAGAGTCAGTGAAGCAACCCCTTA 506
|||||
Db 361 AGGACACAGCACACACAGCGGCTGAGCGGAGCAATCTTAGAGTCAGTGAAGCAACCCCTTA 420
|||||
QY 507 TTGTGGAAGTGGGCTATGCTTCAGAGTGTGGCAACTCTACATCTTGAAGTCC 566
|||||
Db 421 TTGTGGAAGTGGGCTATGCTTCAGAGTGTGGCAACTCTACATCTTGAAGTCC 480
|||||
QY 567 TCAGTGTGGCGAGCTCTTCAGGCAATCTGAGGAGAGGAGCAATCTTCGGAAGATAGG 626
|||||
Db 481 TCAGTGTGGCGAGCTCTTCAGGCAATCTGAGGAGAGGAGCAATCTTCGGAAGATAGG 540
|||||
QY 627 CTTGCTTACCTGAGCTGAGATCACGCTGCGCCCTGGCCATCTCCACTCCAGGGCATCA 686
|||||
Db 541 CTTGCTTACCTGAGCTGAGATCACGCTGCGCCCTGGCCATCTCCACTCCAGGGCATCA 600
|||||
QY 687 TCTACCGGAGCTCAAGCCCGAGACATATGCTACGACGCCAGGGCCCATCAAACTCA 746
|||||
Db 601 TCTACCGGAGCTCAAGCCCGAGACATATGCTACGACGCCAGGGCCCATCAAACTCA 660
|||||
QY 747 CCGACTTGGAGCTCTCAAGAGATCTATCATGAGGGGCCCGTCACTACACTTCTGCG 806
|||||
Db 661 CCGACTTGGAGCTCTCAAGAGATCTATCATGAGGGGCCCGTCACTACACTTCTGCG 720
|||||
QY 807 GCACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 866
|||||
Db 721 GCACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
|||||
QY 867 ACTGCTGAGAGCTG -GGGGCCCTGATGATGATGATGATGATGATGATGATGATGATGATG 924
|||||
Db 781 ACTGCTGAGAGCTGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 840
|||||
QY 925 CGGAGAGACCGGAG 979
|||||
Db 841 CGGAG 900
|||||
QY 980 CCCCCTACCTACCCAGATGCCCCGGG 1007
|||||
Db 901 CCCCCTACCTACCCAGATGCCCCGGG 928
|||||
RESULT 14
BQ062171 1075 bp mRNA linear EST 02-APR-2002
LOCUS AGENCOURT 6829901 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5923618
DEFINITION 5', mRNA sequence.
ACCESSION BQ062171
VERSION BQ062171.1 GI:19888767
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.mc.man.ac.uk/1 (bases 1 to 1075)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2002, 00:20:51 ; Search time 277 Seconds
(without alignments)
14764.003 Million cell updates/sec

Title: US-09-762-258-1

Perfect score: 1816
Sequence: 1 gagagagagagagagagaga.....aaaaaaaaaaaaaaaa 1816

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: N_Geneseq_101002.*

```
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1816	100.0	1816	21	AAZ50703	p70(beta) S6 kinase
2	1724	94.9	1732	24	AAD37031	Human p54S6k DNA.
3	1531.2	84.3	1647	21	AAZ87838	Human serine/threo
4	1158.6	63.8	1197	21	AAZ21858	Human breast and o
5	1104.4	60.8	1637	20	AAZ61282	Human signal pepti
6	720	39.6	1607	21	AAZ87837	Human serine/threo
7	720	39.6	1609	21	AAZ35657	Human serine/threo
8	619.8	34.1	2346	24	ABL5827	Lung cancer relate
9	514	28.3	1898	23	ABL16561	Drosophila melanog

10	514	28.3	2556	19	AAV19873	Drosophila p70S6K
11	455.6	25.1	843	22	AAH77989	Partial nucleotide
12	422.2	23.2	4357	22	AAK86891	Human immune/haema
13	422.2	23.2	6923	22	AAK86892	Human immune/haema
14	418.8	23.1	475	24	ABK64273	Human benign prost
15	371	20.4	673	21	AAZ15983	Human prostate can
16	337	18.6	2791	20	AAZ09173	Human rsk3 CDNA.
17	337	18.6	2791	20	AAZ84493	p90 ribosomal S6 k
18	337	18.6	5673	24	AAZ94865	Human DNA sequence
19	332.4	18.3	3061	24	ABK83808	Human cDNA differe
20	332.4	18.3	3061	24	ABN95648	Gene #2146 used to
21	331.2	18.2	413	24	ABN93683	Gene #181 used to
22	305.8	16.8	594	23	AAZ19264	Human cDNA encodin
23	298.4	16.4	1230	23	AAZ84869	DNA encoding novel
24	297.2	16.4	3131	21	AAZ10533	Mitogen and stress
25	297.2	16.4	3400	22	AAZ51952	Human polynucleoti
26	294.6	16.2	2116	21	AAZ10542	Mitogen and stress
27	294.6	16.2	2117	21	AAZ10530	Mitogen and stress
28	294.6	16.2	2134	21	AAZ10531	Mitogen and stress
29	294.6	16.2	2134	21	AAZ10543	Mitogen and stress
30	290.8	16.0	2222	21	AAZ10532	Mitogen and stress
31	288.2	15.9	3132	22	AAZ52936	Human polynucleoti
32	288.2	15.9	3165	23	AAZ84870	DNA encoding novel
33	263	14.5	2955	24	ABL39746	Human NS cDNA sequ
34	260.8	14.4	1443	24	ABL50837	Human Akt1 encodin
35	260.8	14.4	2181	19	AAV71037	PKB-green flouresc
36	260.8	14.4	2184	19	AAV71086	Green fluorescent
37	260.8	14.4	2610	18	AAZ64812	Human RAC protein
38	260.8	14.4	2610	18	AAZ67135	Human RAC protein
39	260.8	14.4	2610	20	AAZ41177	Human Akt-1 encodi
40	260.8	14.4	2610	20	AAZ22190	Human Akt-1 DNA se
41	260.8	14.4	2610	21	AAZ09076	Wild type human Ak
42	260.8	14.4	2610	24	ABK84055	Human cDNA differe
43	260.8	14.4	2610	24	AAZ28548	Human Akt cDNA #1.
44	259	14.3	2626	21	AAZ09078	Wild type murine A
45	259	14.3	2626	24	AAZ28550	Mouse Akt cDNA. M

ALIGNMENTS

RESULT 1	AAZ50703	AAZ50703 standard; DNA; 1816 BP.
ID	AAZ50703	
AC	AAZ50703;	
XX		
DT	31-MAY-2000 (first entry)	
XX		
DE	p70(beta) S6 kinase gene.	
KW	p70 (beta) S6 kinase; p70betas6k; ribosomal protein kinase; S6 protein;	
KW	cellular signalling; probe; ribosomal activity; cellular proliferation;	
KW	cytosolic; ss.	
XX		
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
FT	77..1564	
FT	/*tag= a	
FT	/product= "p70(beta) S6 kinase"	
FT	1..66	
FT	repeat_region	
FT	/*tag= b	
FT	/label= GA_repeat	
FT	/rpt_type= TANDEM	
FT	/note= "Modulates translation initiation"	
FT	1..2	
FT	/*tag= c	
FT	/label= GA_repeat	
PN	WO200008173-A1.	
XX		
PD	17-FEB-2000.	

Db	1621	AGCAGGACCCCTGGGCCAATTCCAGAGACTGGGGGTGTGTCTCGGGGTGGGGTGTGA	1680
Oy	1681	CGTAGAAAGTGTCGTCTGCTGGGGCAGCTGTCGCCCTGAATCATGGGCAGAGGGCC	1740
Dd	1681	CGTAGAAAGTGTCGTCTGCTGGGGCAGCTGTCGCCCTGAATCATGGGCAGAGGGCC	1740
Oy	1741	GCCCCCAGCACCCCGCGCTCAACTCTCTCCCTGGAGAATTAAAGGCTGAATCATGAAAA	1800
Dd	1741	GCCCCCAGCACCCCGCGCTCAACTCTCTCCCTGGAGAATTAAAGGCTGAATCATGAAAA	1800
Oy	1801	AAAAAAAAAAAAAAAAA 1816	
Dd	1801	AAAAAAAAAAAAAAAAA 1816	
 RESULT 2 AAD37031 ID AAD37031 standard; DNA; 1732 BP.			
XX	AAD37031;		
XX	AC		
XX	DT		
XX	27-AUG-2002 (first entry)		
DE	Human p54S6K DNA.		
KW	Human; mammalian kinase; p54S6K; p85S6K; antibody generation; cancer;		
KW	diagnosis; drug identification; cytostatic; enzyme; gene; ds.		
OS	Homo sapiens.		
XX			
XX	Key	Location/Qualifiers	
FH	CDS	36..1484	
FT		/*tag= a	
FT		/product= "Human p54S6k protein"	
XX			
PN	US6372467-B1.		
XX			
PD	16-APR-2002.		
XX			
PF	29-OCT-1999; 99US-0430564.		
XX			
PR	29-OCT-1998; 98US-106141P.		
XX			
PA	(HARD) HARVARD COLLEGE.		
XX			
PI	Blenis J, Lee-fruman KK, Kuo CJ.		
XX			
DR	WPI; 2002-424732/45.		
DR	P-PSDB; AAE23306.		
XX			
PT	Isolated mammalian p54S6K and p85S6K kinases, useful for diagnosing and		
PT	treating cancers -		
XX			
XX	Example 1; Fig 1A; 30pp; English.		
PS			
XX			
CC	The invention relates to mammalian kinases, p54S6K and p85S6K and		
CC	methods for identifying compounds that modulate, or which are modulated		
CC	by p54S6K and p85S6K. The p54S6K and p85S6K kinases may be used as		
CC	antigens to generate antibodies that may be used in immunoassays to		
CC	detect and quantitate the presence of p54S6K and p85S6K kinases in		
CC	samples and therefore be used to diagnose diseases, e.g. cancers. They		
CC	may also be used in assays as drug targets to identify potential drugs		
CC	for the treatment of diseases associated with p54S6K and p85S6K kinase		
CC	expression and activity. The present sequence is human p54S6K DNA.		
XX			
SQ	Sequence 1732 BP; 355 A; 532 C; 532 G; 313 T; 0 other;		
 Query Match 94.9%; Score 1724; DB 24; Length 1732; Best Local Similarity 100.0%; Pred. No. 0; Matches 1724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Oy	89	CGACGGGCCCCGGGGGCGCGCCGCCCATAGCGGCCGCTTTGATTGGATTGGAGACG	148

Db	9	CGACGGGCCCCCGGGGCCGGCCGCGCATGCGGCCGTGTGGATTGTGGATTTGGAAACG	68
Qy	149	GAGGAAAGGCAAGCGAGGGCGAGGGCGAGCCAGAGACTATAGCCCCCGGAGCAGCATGTGCCCTT	208
Db	69	GAGGAAGGCAAGCGAGGGCGAGGGCGAGCCAGAGCTATAGCCCCGGGAGCAGCATGTGCCCTT	128
Qy	209	GCCGAGTTGAGGGCAGCTGGCCTTAGAGACCTGTGTGGACACTATGAAGAGGTGGAGCTACT	268
Db	129	GCCGAGTTGAGGGCAGCTGGCCTTAGAGACCTGTGTGGACACTATGAAGAGAGTGGAGCTACT	188
Qy	269	GAGACACGCGTGAACGTGTGGCCCAAGAGCGATGGGGCCCACTGCTTGTAGCTGTGGCT	328
Db	189	GAGACACGCGTGAACGTGTGGCCCAAGAGCGATGGGGCCCACTGCTTGTAGCTGTGGCT	248
Qy	329	GTCGTGGGCAAGGGGGGCTATGGCAAGGTGTTCACAGTCCGAAAGGTGCAGAGCCAAAC	388
Db	249	GTCGTGGGCAAGGGGGGCTATGGCAAGGTGTTCACAGTCCGAAAGGTGCAGAGCCAAAC	308
Qy	389	TTGGGCAAAATATATATGCCATGAAGTCTTAGAGAGGCCAAAAATGTGGCAATGCCAAG	448
Db	309	TTGGGCAAAATATATATGCCATGAAGTCTTAGAGAGGCCAAAAATGTGGCAATGCCAAG	368
Qy	449	GACACAGCACACACAGGGGCTGAGCGGGAATATCTTAGACTCAGTGAAGCAACCCCTTATT	508
Db	369	GACACAGCACACACAGGGGCTGAGCGGGAATATCTTAGACTCAGTGAAGCAACCCCTTATT	428
Qy	509	GTCGAACCTGGGCTATATGCTTTCAGAGCTGGGGCAAACTCTACCTCATCCTTTAGAGCCTC	568
Db	429	GTCGAACCTGGGCTATATGCTTTCAGAGCTGGGGCAAACTCTACCTCATCCTTTAGAGCCTC	488
Qy	569	AGTGTGGCGAGCTTCTTACAGCATCTTGAGCGAGAGGGCATCTTCTGTGAAGATACGGCC	628
Db	489	AGTGTGGCGAGCTTCTTACAGCATCTTGAGCGAGAGGGCATCTTCTGTGAAGATACGGCC	548
Qy	629	TGCTTTACCTGGCTGAGATCAGGCTGTGGCCCTGGGCATCTCCACTCCGAGGGCATATC	688
Db	549	TGCTTTACCTGGCTGAGATCAGGCTGTGGCCCTGGGCATCTCCACTCCGAGGGCATATC	608
Qy	689	TACCGGAGCTCAAGCCCCGAGAACATCATCTCAGAGGCGAGGGCCACATCAAACTGAC	748
Db	609	TACCGGAGCTCAAGCCCCGAGAACATCATCTCAGAGGCGAGGGCCACATCAAACTGAC	668
Qy	749	GACTTTGGACTCTCAGAGGAGTATTCATCAGAGGGGCGCGTCACTTCACACTTCTGCGGC	808
Db	669	GACTTTGGACTCTCAGAGGAGTATTCATCAGAGGGGCGCGTCACTTCACACTTCTGCGGC	728
Qy	809	ACCATTTAGTACATGGCCCCCTGAGATTCTGTGCGCAGTGGCCACACCGGGCTGTGAC	868
Db	729	ACCATTTAGTACATGGCCCCCTGAGATTCTGTGCGCAGTGGCCACACCGGGCTGTGAC	788
Qy	869	TGTGTGAGACCTGGGGGGCCCGATGTACGATGCTCAATGAGANTCGCGGCCCTTACCGCA	928
Db	789	TGTGTGAGACCTGGGGGGCCCGATGTACGATGCTCAATGAGANTCGCGGCCCTTACCGCA	848
Qy	929	GAGAACCGGAGAAACCATGATTAAGATCATAGGGGCAAGCTGTGCACTGTGCCCTTAC	988
Db	849	GAGAACCGGAGAAACCATGATTAAGATCATAGGGGCAAGCTGTGCACTGTGCCCTTAC	908
Qy	989	CTCACCCCAAGATGCCCGGAGACTTGTCAAAAATTTCTGAAACGGAATCCAGCCAGGG	1048
Db	909	CTCACCCCAAGATGCCCGGAGACTTGTCAAAAATTTCTGAAACGGAATCCAGCCAGGG	968
Qy	1049	ATTGGGGGTGGCCCAAGGGAGATGTGTGTGATGTCAAGAGCATCCCTTTTCCGGCAATG	1108
Db	969	ATTGGGGGTGGCCCAAGGGAGATGTGTGTGATGTCAAGAGCATCCCTTTTCCGGCAATG	1028
Qy	1109	AATTGGAGAGCACTTCTTGAGCTTGCGCTGTGTGAGACCCCTTTCAGGCGCTGTGTGAGTCA	1168
Db	1029	AATTGGAGAGCACTTCTTGAGCTTGCGCTGTGTGAGACCCCTTTCAGGCGCTGTGTGAGTCA	1088
Qy	1169	GAGGAGAGCTGAGCAGTTTGTATACCGCTTCACAGCGAGCAGCGGCTGGACAGTCTT	1228

D	b	1089	GAGAGGACGTGAGCCAGCTTTGATTACCCGCTTCACACGGCAGAACCCCGGTGACAGTCT	1148
Q	y	1229	GATGACACAGCCCTCAGCCAGAGTGTCCAAACAGAGCCCTTCTGGGCTTCACATACGTGGC	1288
D	b	1149	GATGACACAGCCCTCAGCCAGAGTGTCCAAACAGAGCCCTTCTGGGCTTCACATACGTGGC	1208
Q	y	1289	CCGTCTCTCCGTGAGACGATCAAGAGAGGGCTTCTCTTCACACCCCAACCTGCGTCACACC	1348
D	b	1209	CCGTCTCTCTCCGTGAGACGATCAAGAGAGGGCTTCTCTTCACACCCCAACCTGCGTCACACC	1268
Q	y	1349	AGGGCCCTCAACAGTATAGCCCTCCGGATCCCGTCAGCCCTCAAGTTCCTCCCTTTTGAG	1408
D	b	1269	AGGGCCCTCAACAGTATAGCCCTCCGGATCCCGTCAGCCCTCAAGTTCCTCCCTTTTGAG	1328
Q	y	1409	GGGTTTGGGCCACAGCCCAAGCCTGTCGGGAGACCCAGGAGTCACTTCACACTCTG	1468
D	b	1329	GGGTTTGGGCCACAGCCCAAGCCTGTCGGGAGACCCAGGAGTCACTTCACACTCTG	1388
Q	y	1469	CCACCGCGCGCGCCTGTGACACAGCGCCCTCTCCCTCCGTCGCCCTCTAGGAGACAG	1528
D	b	1389	CCACCGCGCGCGCCTGTGACACAGCGCCCTCTCCCTCCGTCGCCCTCTAGGAGACAG	1448
Q	y	1529	AAGTCCAAAGAGGGCCGTGTGGCGCTCCAGGGCGCTAGAGAACCGGGTGGGGGTGAGGTAG	1588
D	b	1449	AAGTCCAAAGAGGGCCGTGTGGCGCTCCAGGGCGCTAGAGAACCGGGTGGGGGTGAGGTAG	1508
Q	y	1589	CCCTTGAAGCCCTGTCTCTGCGGCTGTGAGACGACGAGACCTGGGCAAGTTCACAGAC	1648
D	b	1509	CCCTTGAAGCCCTGTCTCTGCGGCTGTGAGACGAGACCTGGGCAAGTTCACAGAC	1568
Q	y	1649	CTGGGGGGGTGTCTGGGGGGTGGGGGTGTGAGTGGTGTGAATGTGTGTCTGTGGGGCA	1708
D	b	1569	CTGGGGGGGTGTCTGGGGGGTGGGGGTGTGAGTGGTGTGAATGTGTGTCTGTGGGGCA	1628
Q	y	1709	GCTGTGCCCTGGAATCATGTGGCAAGGAGGGCCGCCGACACCCCGGCTCAACTGTCTC	1768
D	b	1629	GCTGTGCCCTGGAATCATGTGGCAAGGAGGGCCGCCGACACCCCGGCTCAACTGTCTC	1688
Q	y	1769	CCGTGTGAAGATTAAAGGGCTGAATCATGAAAAAAAAAAAAAAAAAAAAA	1812
D	b	1689	CCGTGTGAAGATTAAAGGGCTGAATCATGAAAAAAAAAAAAAAAAAAAAA	1732

RESULT_3	
AAZ87838	
ID	AAZ87838 standard; cDNA; 1647 BP.
XX	
AC	AAZ87838;
XX	
DT	19-JUN-2000 (first entry)
XX	
DE	Human serine/threonine protein kinase (HSTK)-3 encoding cDNA.
XX	
KW	Serine/threonine protein kinase; HSTK; cancer; leukemia; testicular;
KW	melanoma; inflammatory disease; asthma; atherosclerosis; aniridia;
KW	diabetes mellitus; growth disorder; anemia; achondroplastic dwarfism;
human; HSTK-3; ss.	
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	389..1405
CDS	
FT	/*tag= a
FT	/product= "HSTK-3"
XX	
PN	WO200015770-A2.
XX	
PD	23-MAR-2000.
XX	
PF	16-SEP-1999; 99WO-US21595.
XX	
PR	16-SEP-1998; 98US-0153939.
XX	

PA (INCY-) INCYTE PHARM INC.
 XX
 XX Bandman O, Tang YT, Goli SK, Corley NC, Guegler KJ, Gorgone GA,
 PI Hillman JL,
 XX
 DR WPI: 2000-271413/23.
 DR P-PSDB: AAY77845.
 XX
 XX Human serine/threonine protein kinases useful in the prevention,
 PT diagnosis and treatment of cancers, inflammatory diseases and disorders
 PT that affect growth and development -
 XX
 PS Claim 9, Fig 2A-E; 73pp; English.
 XX
 XX The invention relates to human serine/threonine protein kinase (HSTK)-3
 CC polypeptides and the nucleic acids that encode them. The HSTK-3 protein
 CC can be expressed by standard recombinant methodology. The HSTK-3
 CC polypeptides may be used as antigens in the production of antibodies
 CC against hSTK-3 and in assays to identify modulators (agonists and
 CC antagonists) of hSTK-3 expression and activity. The HSTK-3 specific
 CC antibodies and modulators can be used to treat disorders such as cancers
 CC (e.g. leukemia, testicular cancer and melanomas), inflammatory diseases
 CC (e.g. asthma, atherosclerosis and diabetes mellitus) and disorders that
 CC affect growth and development (e.g. anemata, achondroplastic dwarfism and
 CC aniridia). The anti-hSTK-3 antibodies may also be used as diagnostic
 CC agents for detecting the presence of HSTK-3 polypeptides in samples (e.g.
 CC by enzyme linked immunosorbant assay (ELISA)). The present sequence
 CC represents a cDNA encoding a HSTK-3 polypeptide.
 XX
 XX Sequence 1647 BP; 334 A; 507 C; 505 G; 299 T; 2 other;

Query Match	Similarity	84.3%	Score 1531.2	DB 21	Length 1647
Best Local	Similarity	95.3%	Pred. Num. 0	Mismatches 10	Indels 71
Matches 1637	Conservative	0	No. Matches	10	Indels 71
					Gaps 3
QY	89	GCACGCCCCCGGGGGCCGCGCCGCCCAAGCGGCGCCGTGTTGATTGATTGGAGACG	148		
DB	1	CGACGGCCCCCGGGGGCGC-----CGCATGGCGCNGNNGTGTGATTGATTGGAGACG	56		
QY	149	GAGGAAGCGAGGAGGGCGAGGGCGAGGCCAGACGCTCAGCCCGCGGAGCCCATGTCCCTT	208		
DB	57	GAGGAAGCGAGGAGGGCGAGGGCGAGGCCAGACGCTCAGCCCGC-----	101		
QY	209	GCCGAGTTGAGGGCAGCTGGCCCTAGAGCCCTGTGGGACATATGAAAGGTGAGCTGACT	268		
DB	102	-----GCTGTGGGACATATGAAGAGGTGAGCTGACT	135		
QY	269	GAGACCAGCGTAAACGTTGGCCAGAGCGCATCGGGCCCCACTGCTTAACTGCTGCGT	328		
DB	136	GAGACCAGCGTAAACGTTGGCCAGAGCGCATCGGGCCCCACTGCTTAACTGCTGCGT	195		
QY	329	GTCGTGGCGAAGGGGGGCTATGCAAGAGTGTTCCAGGTCCGAAGGTGCAAGGACACAC	388		
DB	196	GTCGTGGCGAAGGGGGGCTATGCAAGAGTGTTCCAGGTCCGAAGGTGCAAGGACACAC	255		
QY	389	TTGGGCAAAATATATGCCATTAAGTCTTAAGGAAGGCCAAAATTGTCGCCAATGCCAAG	448		
DB	256	TTGGGCAAAATATATGCCATTAAGTCTTAAGGAAGGCCAAAATTGTCGCCAATGCCAAG	315		
QY	449	GACACAGCACACACGCGGCTGAGGGGAACATTTTCAAGTCAAGTGAAGACACCCCTTATT	508		
DB	316	GACACAGCACACACGCGGCTGAGGGGAACATTTTCAAGTCAAGTGAAGACACCCCTTATT	375		
QY	509	GTTGAATGCGCTATGCTTCCAGACTGGTGGCAAACTCTACCTCATCTTGAAGTGCCTC	568		
DB	376	GTTGAATGCGCTATGCTTCCAGACTGGTGGCAAACTCTACCTCATCTTGAAGTGCCTC	435		
QY	569	AGTGTGGCGACCTCTTACGCATCTGGAGCGAGGCGCATCTCTCTGGAAGATAGGGCG	628		
DB	436	AGTGTGGCGACCTCTTCTG-----GGAAGATAGGGCG	469		
QY	629	TGCTTCTACCTGGCTGAGATACAGCTGGCGCTTGGGCATCTCACATCCAGGGCATATC	688		

```

Db 470 TGTCTTCACTGCTGAGATCACGCTGGCCCTGGGCCATCTCCACTCCAGGCGATCATC 529
QY 689 TACCGGAGCTCAAGCCCGAGACATCATGCTCAGACAGCCAGGGCGACATGAAACTGACC 748
Db 530 TACCGGAGCTCAAGCCCGAGACATCATGCTCAGACAGCCAGGGCGACATGAAACTGACC 589
QY 749 GACTTTGGACTCTGCAAGAGTCTATCCATGAGGGCGCCGTCACATCACCCTTGTGCGGC 808
Db 590 GACTTTGGACTCTGCAAGAGTCTATCCATGAGGGCGCCGTCACATCACCCTTGTGCGGC 649
QY 809 ACCATTGAGTACATGCCCCCTGAGATTCTGTGCGCAGTGGCCACACCCGGCTGTGAC 868
Db 650 ACCATTGAGTACATGCCCCCTGAGATTCTGTGCGCAGTGGCCACACCCGGCTGTGAC 709
QY 869 TGGAGGAGCCCTGGGGGCCCTGATGAGACATGCTCATGTGATGGCGCCCTTAAACGCA 928
Db 710 TGGTGGAGCCCTGGGGGCCCTGATGAGACATGCTCATGTGATGGCGCCCTTAAACGCA 769
QY 929 GAGAACCGGAGAAAGAACCATGATAGATCATCAGGGGCAAGCTGGCAGTCCGCCCTTAC 988
Db 770 GAGAACCGGAGAAAGAACCATGATAGATCATCAGGGGCAAGCTGGCAGTCCGCCCTTAC 829
QY 989 CTCACCCCGATGCCCCGGGACCTTGTCAAAAAGTTTCTGAACGGAATCCAGCCAGCGG 1048
Db 830 CTCACCCCGATGCCCCGGGACCTTGTCAAAAAGTTTCTGAACGGAATCCAGCCAGCGG 889
QY 1049 ATTGGGGGTGGCCCGAGGGAGTGTCTGTATGTGACAGACATFCCCTTTTCCGACATG 1108
Db 890 ATTGGGGGTGGCCCGAGGGAGTGTCTGTATGTGACAGACATFCCCTTTTCCGACATG 949
QY 1109 AATTGGGACGACCTTGTGAGCTGTGGAGTGGACCCCTTTCAGAGCCCTGTCTGTGACATCA 1168
Db 950 AATTGGGACGACCTTGTGAGCTGTGGAGTGGACCCCTTTCAGAGCCCTGTCTGTGACATCA 1009
QY 1169 GAGAGAGACGTGAGCCAGTTTGATACCCGCTTCACAGCGCAGACGCCGGTGACAGTCTT 1228
Db 1010 GAGAGAGACGTGAGCCAGTTTGATACCCGCTTCACAGCGCAGACGCCGGTGACAGTCTT 1069
QY 1229 GATGACACAGCCCTCAGGAGAGAGTGGCCAAAGAGCCCTTCGAGGCTTACATACGTGGCG 1288
Db 1070 GATGACACAGCCCTCAGGAGAGAGTGGCCAAAGAGCCCTTCGAGGCTTACATACGTGGCG 1129
QY 1289 CCGTCTGCTCTGACAGCATCAAGAGAGGCTTCTCCATCCAGCCCAAGCTCGCTCACCC 1348
Db 1130 CCGTCTGCTCTGACAGCATCAAGAGAGGCTTCTCTCTCCAGCCCAAGCTCGCTCACCC 1189
QY 1349 AGGCGCCTCAACAGTAGGCCCGGGGTCCCGCTCAGGCCCTCAAGTCTCCCTTTTGTAG 1408
Db 1190 AGGCGCCTCAACAGTAGGCCCGGGGTCCCGCTCAGGCCCTCAAGTCTCCCTTTTGTAG 1249
QY 1409 GGGTTTGGGCCCCAGCCCGAGCTGTGCGGAGCCCAAGAGTACCTCTACCTCCACTCTG 1468
Db 1250 GGGTTTGGGCCCCAGCCCGAGCTGTGCGGAGCCCAAGAGTACCTCTACCTCTCTCTG 1309
QY 1469 CCACCGCGCGCCCTCTGACACAGCGCCCTCTCCCATCTCCCTCCCTCAGAGGACAAAG 1528
Db 1310 CCACCGCGCGCCCTCTGACACAGCGCCCTCTCCCATCTCCCTCCCTCAGAGGACAAAG 1369
QY 1529 AAGTCCAAAGAGGGGCGGTGGCGCTCAAGGGCGCTAGGAAGCCGGGTGGGGGTGAGGATG 1588
Db 1370 AAGTCCAAAGAGGGGCGGTGGCGCTCAAGGGCGCTAGGAAGCCGGGTGGGGGTGAGGATG 1429
QY 1589 CCCTTGAGACCTCTGTCCCTGCGGCTGTGAGACAGAGAGACCTTGGGCCAAGTTCCAGAAAC 1648
Db 1430 CCCTTGAGACCTCTGTCCCTGCGGCTGTGAGACAGAGAGACCTTGGGCCAAGTTCCAGAAAC 1489
QY 1649 CTGGGGGTGTGTCTGGGGGTGGGGGTGATGAGTAAAGTGTGTCTGTCTGGGGCA 1708
Db 1490 CTGGGGGTGTGTCTGGGGGTGGGGGTGATGAGTAAAGTGTGTCTGTCTGGGGCA 1549
QY 1709 GCTGTGCCCTGAAATCATGAGGACAGAGAGGCCCGCCGACACCCCGCGCTCAACTGCTC 1768
Db 1550 GCTGTGCCCTGAAATCATGAGGACAGAGAGGCCCGCCGACACCCCGCGCTCAACTGCTC 1609

```

```

QY 1769 CCGTGAAGATTAAAGGCTGATCATGAAAAA 1806
Db 1610 CCGTGAAGATTAAAGGCTGATCATGAAAAA 1647

RESULT 4
AAF21858
ID AAF21858 standard; DNA; 1197 BP.
XX
AC AAF21858;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human breast and ovarian cancer associated antigen gene SEQ ID 245.
XX
KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW neotropic; neurproliferative; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antitumor; vulnery; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease; ds.
XX
OS Homo sapiens.
XX
PN W0200055173-1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05881.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI: 2000-611515/58.
XX
DR P-PSDB: AAB58955.

New human breast and ovarian cancer associated gene sequences and the
PT polypeptides encoded by these genes, useful in the prevention,
PT treatment and diagnosis of cancer, immune disorders, cardiovascular
PT disorders and neurological diseases -
PS
XX
XX
Claim 1: Page 669; 1299pp; English.
CC
CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC associated with breast and ovarian cancer. Included in the invention are
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC isolation and characterisation of the DNA and protein sequences of the
CC invention. The breast and ovarian cancer associated DNA, protein, agonist
CC or antagonist sequences exhibit cytostatic; immunosuppressive;
CC neotropic; neurproliferative; antiviral; antiallergic; hepatotropic;
CC antidiabetic; antiinflammatory; antitumor; vulnery; anticonvulsant;
CC antibacterial; antifungal; antiparasitic and cardiant activity. The
CC polynucleotide and protein sequences are used in the diagnosis of cancer,
CC particularly breast and ovarian cancer. The nucleic acid sequences,
CC proteins, agonists and agonists may also be used in the diagnosis,
CC prevention and treatment of immune disorders e.g. Addison's disease,
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; cardiovascular disorders such as
CC myocardial ischemias; wound healing; neurological diseases such as
CC cerebral anoxia and epilepsy; and infectious diseases.
XX
SO Sequence 1197 BP; 230 A; 396 C; 350 G; 216 T; 5 other;

Query Match 63.8%; Score 1158.6; DB 21; Length 1197;
Best Local Similarity 99.3%; Pred. No. 2.4e-247;

```

Matches 1180;	Conservative 3;	Mismatches 3;	Indels 2;	Gaps 2;
QY 624	CGGCTGCTCTTCTACCTGGCTGAGATCAGCGTGGCCCTGGGCCATCTCCACTGCTCCAGGGCA			683
Db 11	CGGCTGCTCTTCTACCTGGCTGAGATCAGCGTGGCCCTGGGCCATCTCCACTGCTCCAGGGCA			70
QY 684	TCATCTACCGGAGCTTCAGAGCCCGAGACATCATGCTCAGACGCGGACGCGCATCAAC			743
Db 71	TCATCTACCGGAGCTTCAGAGCCCGAGACATCATGCTCAGACGCGGACGCGCATCAAC			130
QY 744	TGACCGACTTTGGAGCTCTGCAAGAGTCTATCATATGAGGCGCGCTACCTCACACCTTCT			803
Db 131	TGACCGACTTTGGAGCTCTGCAAGAGTCTATCATATGAGGCGCGCTACCTCACACCTTCT			190
QY 804	GCGGCACCATTTGAGTACATGAGCCCTG-AGATTCTGCTGGCAGTGGCCCAACCGGGCT			862
Db 191	GCGGCACCATTTGAGTACATGAGCCCTGAGATTCTGCTGGCAGTGGCCCAACCGGGCT			250
QY 863	GTCGACTGCTGGAGCCTGGGGGCGCTGATGTACGACATGCTCACTGGATGCGCCCTT			922
Db 251	GTCGACTGCTGGAGCCTGGGGGCGCTGATGTACGACATGCTCACTGGATGCGCCCTT			310
QY 923	ACCGCAGAGAACCGGAAAGAAACCATGATAGATCATCAGGGGCAAGCTGGCACTGCC			982
Db 311	ACCGCAGAGAACCGGAAAGAAACCATGATAGATCATCAGGGGCAAGCTGGCACTGCC			370
QY 983	CCCTACCTACCCCAAGATGCGCGGACCTTGTCAAAAAGTTTCTGAAACGGAATCCAGC			1042
Db 371	CCCTACCTACCCCAAGATGCGCGGACCTTGTCAAAAAGTTTCTGAAACGGAATCCAGC			430
QY 1043	CACGCGATTGGGGGTGGCCCGAGGGGATGCTGCTGATGTGAGAGACATCCCTTTTCCG			1102
Db 431	CACGCGATTGGGGGTGGCCCGAGGGGATGCTGCTGATGTGAGAGACATCCCTTTTCCG			490
QY 1103	CACATGATTTGGGACGACCTTCTGCGCTGGCGTGGAGACCCCTTTCAGGCCCTGCTG			1162
Db 491	CACATGATTTGGGACGACCTTCTGCGCTGGCGTGGAGACCCCTTTCAGGCCCTGCTG			550
QY 1163	CAGTCAGAGGAGAGCAGTGAAGCCAGTTTGATACCGCTTTCACAGGCGAGACCGCGTGAG			1222
Db 551	CAGTCAGAGGAGAGCAGTGAAGCCAGTTTGATACCGCTTTCACAGGCGAGACCGCGTGAG			610
QY 1223	AGTCGATGACACACAGCCCTCAGAGAGAGTCCACAGGCGCTTCTGGGCTTCACTAC			1282
Db 611	AGTCGATGATACACAGCCCTCAGAGAGAGTCCACAGGCGCTTCTGGGCTTCACTAC			670
QY 1283	GTCGCGCGCTGCTGCTGAGACATCAAGAGAGGCTTCTCTTCCAGGCCCAAGCTGCGC			1342
Db 671	GTCGCGCGCTGCTGCTGAGACATCAAGAGAGGCTTCTCTTCCAGGCCCAAGCTGCGC			730
QY 1343	TCACCCAGGCGCTCAACAGTACCCCGGGGTCCCGTCAAGCCCTCAAGTTCTCCCT			1402
Db 731	TCACCCAGGCGCTCAACAGTACCCCGGGGTCCCGTCAAGCCCTCAAGTTCTCCCT			790
QY 1403	TTTGAAGGGGTTTGGGCGGAGCCGAGCTTGGCCGAGCCGAGAGTACTTACTCTCA			1462
Db 791	TTTGAAGGGGTTTGGGCGGAGCCGAGCTTGGCCGAGAGTACTTACTCTCA			850
QY 1463	CTCTGCAACCGCGCGCTGAGACACCGCGCTCTCCCATCTCCCTCCCTCAAGG			1522
Db 851	CTCTGCAACCGCGCGCTGAGACACCGCGCTCTCCCATCTCCCTCCCTCAAGG			910
QY 1523	ACCAAGAGTCAAGAGAGGGCGCTGGGCGTCAAGGGCGCTAGAGAACCGGGTGGGGTGA			1582
Db 911	ACCAAGAGTCAAGAGAGGGCGCTGGGCGTCAAGGGCGCTAGAGAACCGGGTGGGGTGA			970
QY 1583	GGGTACCCCTTGAGCCCTGCTGCGGCTGTAGAGCAGAGAGACCTTGCGCACTTCC			1642
Db 971	GGGTACCCCTTGAGCCCTGCTGCGGCTGTAGAGCAGAGAGACCTTGCGCACTTCC			1030
QY 1643	AGAGACCTGGGGGTGTGTCTGGGGGTGGGGTGTGATGGTATGAAGGTGTGTGCT			1702
Db 1031	AGAGACCTGGGGGTGTGTCTGGGGGTGGGGTGTGATGGTATGAAGGTGTGTGCT			1090

QY	1703	GGGGGAGCGTGTATCCCTGTAATCATATGGGACGAGGAGGCGCGCCGACACACCCGCGCTCAA			1762
Db	1091	GGGGGAGCGTGTATCCCTGTAATCATATGGGACGAGGAGGCGCGCCGACACACCCGCGCTCAA			1149
QY	1763	CTGCTCCCGTGAAGATTAAAGGCGCTGATCATGAAAAA			1810
Db	1150	CTGCTCCCGTGAAGATTAAAGGCGCTGATCATGAAAAA			1197
RESULT 5					
ID	AA61282				
XX	AA61282 standard; cDNA: 1637 BP.				
AC	AA61282;				
XX					
DT	29-JUL-1999 (first entry)				
XX					
DE	Human signal peptide-containing protein encoding cDNA SEQ ID NO:10.				
XX					
KW	Human; signal peptide-containing protein; SP; cell proliferation;				
XX					
KW	cancer; neuronal disorder; immune response; detection; ss.				
XX					
OS	Homo sapiens.				
XX					
PN	W0924463-A2.				
XX					
PD	20-MAY-1999.				
XX					
PF	04-NOV-1998; 98WO-US23578.				
XX					
PR	07-NOV-1997; 97US-0966316.				
XX					
PA	(INCY-) INCYTE PHARM INC.				
XX					
PI	Au-Young J, Lal P, Mathur P, Murry LE, Reddy R;				
XX					
DR	WPI: 1999-337694/28.				
XX					
PT	cDNA clones encoding signal peptide-containing proteins				
XX					
PS	Claim 4; Page 75-76; 83pp; English.				
XX					
CC	The present sequence represents a human cDNA clone encoding a signal				
CC	peptide-containing protein (SP). SP proteins can be used to stimulate				
CC	cell proliferation or to treat or prevent cancer. SP antagonists are				
CC	also used to treat or prevent cancer, and also for treating or				
CC	preventing neuronal disorders or immune responses. Polynucleotide				
CC	sequences complementary to the SP-encoding polynucleotides are useful				
CC	for the detection of SP-encoding nucleic acid molecules in biological				
CC	samples.				
XX					
SO	Sequence 1637 BP; 342 A; 473 C; 463 G; 332 T; 27 other;				
Query Match					
Best Local Similarity 98.8%; Score 1104.4; DB 20; Length 1637;					
Matches 1196; Conservative 0; Mismatches 7; Indels 8; Gaps 8;					
QY	97	CGCGGGGCGGCGCGCCATGGCGCGCGTGTGATTGATTGGAGACGAGGAAG			156
Db	176	CAGCGGGGCGGCGCGCCATGGCGCGCGTGTGATTGATTGGAGACGAGGAAG			235
QY	157	CAGCGAGGCGAGGCGGAGCCAGAGCTCAGCCCGCGAGAGATGCCCTTGGCGAGTT			216
Db	236	CAGCGAGGCGAGGCGGAGCCAGAGCTCAGCCCGCGAGAGATGCCCTTGGCGAGTT			295
QY	217	GAGGCGAGCTGGCCTTAGAGCCTGTGGGACACTATGAAGAGGTGAGCTACTGAGACAG			276
Db	296	GAGGCGAGCTGGCCTTAGAGCCTGTGGGACACTATGAAGAGGTGAGCTACTGAGACAG			355
QY	277	CGTGAACGTTGGGCCCGAGACCGATCGGGCCCACTCTTTGAGACCTGCTGTGTGGG			336
Db	356	CGTGAACGTTGGGCCCGAGACCGATCGGGCCCACTCTTTGAGACCTGCTGTGTGGG			415

```

OY 337 CAAGGGGGCTATGCGAAGGTGTCAGGTGCGAAAGGTGCAAGGCACCAACTTGGGCAA 396
    |||
DB 416 CAAGGGGGGCTATGCGAAGGTGTCAGGTGCGAAAGGTGCAAGGCACCAACTTGGGCAA 475
OY 397 AATATATGCCATGAAGAGTCTTAAGAGAGGCCAAAATTTGCGCAATGCCAAGACACAGC 456
    |||
DB 476 AATATATGCCATGAAGAGTCTTAAGAGAGGCCAAAATTTGCGCAATGCCAAGACACAGC 535
OY 457 ACACACAGGGGCTGAGCGGAGACATCTAGAGTCACTGAAGACCCCTTATTTGTGGAAGT 516
    |||
DB 536 ACACACAGGGGCTGAGCGGAGACATCTAGAGTCACTGAAGACCCCTTATTTGTGGAAGT 595
OY 517 GGGCTATGCTTCCAGACTGGTGGCAAACTTACCTCACTCCTT -GAGTCCCTCAGTGGG 575
    |||
DB 596 GGGCTATGCTTCCAGACTGGTGGCAAACTTACCTCACTCCTTGGATTTGCTCCTCAGTGG 655
OY 576 GCGAGCTCTTCAAGCATCTGAGCGAGAGGGGCAATCTTCTGGAAGATACGGCTCTCTCT 635
    |||
DB 656 GCGAGCTCTTCAAGCATCTGAGCGAGAGGGGCAATCTTCTGGAAGATACGGCTCTCTCT 715
OY 636 ACCTGCTGAGATCAACGCTGGGCTGGGCAATCTCCTCCTCCAGGGCATCATCTACCGGG 695
    |||
DB 716 ACCTGCTGAGATCAACGCTGGGCTGGGCAATCTCCTCCTCCAGGGCATCATCTACCGGG 775
OY 696 ACCTCAAGCCCGAGAAATCATGCTCAGACGCGAGGGCCACATCAAACTGAGCCGACTTTG 755
    |||
DB 776 ACCTCAAGCCCGAGAAATCATGCTCAGACGCGAGGGCCACATCAAACTGAGCCGACTTTG 835
OY 756 GACTCTGCAAGAGATCTATCCATGAGAGGGGCGCTCCTCCTCCTCCTGCGGACCATTTG 815
    |||
DB 836 GACTCTGCAAGAGATCTATCCATGAGAGGGGCGCTCCTCCTCCTCCTGCGGACCATTTG 895
OY 816 AGTAAATGGCCCCCTGAGATCTGCTGCGAGTGGCCACACCGGGCTGTGGACTGTGGA 875
    |||
DB 896 AGTAAATGGCCCCCTGAGATCTGCTGCGAGTGGCCACACCGGGCTGTGGACTGTGGA 955
OY 876 GCGTGGGGGCTGATGATGACGATGCTCAGATGCGGCGGCTTTTACCGAGAGAAAC 935
    |||
DB 956 GCGTGGGGGCTGATGATGACGATGCTCAGATGCGGCGGCTTTTACCGAGAGAAAC 1015
OY 936 GGAAGAAAACATGATGATGATGATGAGGGGCAAGCTGGCACTGGCCCTTACCTACCC 995
    |||
DB 1016 GGAAGAAAACATGATGATGATGATGAGGGGCAAGCTGGCACTGGCCCTTACCTACCC 1075
OY 996 CAGATGCCCCGGGACCTTGTCAAAAAGTTCTGAACGGAATCCAGCCAGCGGATTGGGG 1055
    |||
DB 1076 CAGATGCCCCGGGACCTTGTCAAAAAGTTCTGAACGGAATCCAGCCAGCGGATTGGGG 1135
OY 1056 GTGGGCCAGGGGATGCTGCTGATGTCAGAGAGATCCCTTTTTCGGGCAATGAATTGGG 1115
    |||
DB 1136 GTGGGCCAGGGGATGCTGCTGATGTCAGAGAGATCCCTTTTTCGGGCAATGAATTGGG 1195
OY 1116 AGACCTTCTGGCTGGGCTGTGAGACCCCTTTC -AGGCCCTGTCTGCAAGTCAAGAGAG 1174
    |||
DB 1196 AGCA-CTTCTGGCTGGGCTGTGAGAGCCCTTTCAGAGCCCTGTCTGAGTCAAGAGAG - 1253
OY 1175 GACGTGAGCAATTTGATACCCGCTTTCAGACGCGAGAGCGCGGTGAGCACTGTGATGAC 1234
    |||
DB 1254 GACGTGAGCAATTTGATACCCGCTTTCAGACGCGAGAGCGCGGTGAGCACTGTGATGAC 1312
OY 1235 ACAGCCCTCAGGAGAGTCCCAACAGGCGCTTCTGGGCTTCAATGATGAGCGCGGT 1294
    |||
DB 1313 ACAG-CTTCAAGGAGAGTCCCAACAGGCGCTTCTGGGCTTCAATGATGAGCGCG -GTCT 1369
OY 1295 GTCTGTGAGAG 1305
    |||
DB 1370 GTCTGTGAGAG 1380

```

RESULT 6
AAZ87837
ID AAZ87837 standard; cDNA; 1607 BP.

```

XX AC AAZ87837;
XX AC 19-JUN-2000 (first entry)
XX DE Human serine/threonine protein kinase (HSTK)-2 encoding cDNA.
XX KW Serine/threonine protein kinase; HSTK; cancer; leukemia; testicular;
XX KW melanoma; inflammatory disease; asthma; atherosclerosis; aniridia;
XX KW diabetes mellitus; growth disorder; anemia; achondroplastic dwarfism;
XX KW human; HSTK-3; HSTK-2; ss.
XX OS Homo sapiens.
XX FH Key
XX FH CDS
XX FH Location/Qualifiers
    /tag=a
    /transl_except=(pos:125..127, aa: Xaa)
    /transl_except=(pos:140..142, aa: Xaa)
    /transl_except=(pos:152..154, aa: Xaa)
    /transl_except=(pos:200..202, aa: Xaa)
    /transl_except=(pos:209..211, aa: Xaa)
    /transl_except=(pos:221..223, aa: Xaa)
    /transl_except=(pos:224..226, aa: Xaa)
    /transl_except=(pos:290..292, aa: Xaa)
    /transl_except=(pos:296..298, aa: Xaa)
    /transl_except=(pos:305..307, aa: Xaa)
    /transl_except=(pos:314..316, aa: Xaa)
    /product="HSTK-2"
    /note="Xaa = unknown"

W0200015770-A2.
23-MAR-2000.
16-SEP-1999; 99WO-US21595.
16-SEP-1998; 98US-0153939.
(INCY-) INCYTE PHARM INC.

Bandman O, Tang YT, Goli SK, Corley NC, Guegler KJ, Gorgone GA;
Hillman JL;
WPI: 2000-271413/23.
P-PSDB; AAY77844.

Human serine/threonine protein kinases useful in the prevention,
diagnosis and treatment of cancers, inflammatory diseases and disorders
that affect growth and development -
Disclosure: fig 1A-E; 73pp; English.

PS The invention relates to human serine/threonine protein kinase (HSTK)
XX polypeptides and the nucleic acids that encode them. The HSTK-3
XX can be expressed by standard recombinant methodology. The HSTK-3
XX polypeptides may be used as antigens in the production of antibodies
XX against HSTK-3 and in assays to identify modulators (agonists and
XX antagonists) of HSTK-3 expression and activity. The HSTK-3 specific
XX antibodies and modulators can be used to treat disorders such as cancers
XX (e.g. leukemia, testicular cancer and melanoma), inflammatory diseases
XX (e.g. asthma, atherosclerosis and diabetes mellitus) and disorders that
XX affect growth and development (e.g. anemia, achondroplastic dwarfism and
XX aniridia). The anti-HSTK-3 antibodies may also be used as diagnostic
XX agents for detecting the presence of HSTK-3 polypeptides in samples (e.g.
XX by enzyme linked immunosorbent assay (ELISA)). The present sequence
XX represents a cDNA encoding a HSTK-2 polypeptide.
XX
SQ Sequence 1607 BP; 312 A; 519 C; 472 G; 283 T; 21 other;

```

Query Match 39.6%; Score 720; DB 21; Length 1607;
Best Local Similarity 99.1%; Pred. No. 4.7e-150;
Matches 734; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Db	584	GAGAGGAAATTTATATGGAAGACACTGCTGCTTTTACTTTGGCAGAAATGTCATCGGCTT	643
Qy	660	TGGGCCATCTCCACTCCAGGGCATCTTACCGGGACCTCAAGCCGAGACATCATGC	719
Db	644	TGGGGCATTTTCAATCAAAAGGGGATCATCTTACAGAGACCTGAAGCCGAGAAATATCATGC	703
Qy	720	TCAGAGCCAGGGCCACATCAAACTGACCCGACTTTGGACTCTGCAAGAGACTCATATCAG	779
Db	704	TTAATCACCAAGGATCATGTGAAATTAACAGACTTTGGACTACTGCAAGAAATCTATTCAATG	763
Qy	780	AGGGGGCGGTCACTCACACCTTCTGCGGCACCATTTGAATGATATGCCCCAGATTTCTGG	839
Db	764	ATGGAACAGTCAACACACACATTTTGTGGAACAATAGAAATCATATGGCCCCCTGAATCTTGA	823
Qy	840	TGGCCAGTGGCCACAAACCGGGCTGTGGACTGTGTGGACCTGGGGGCCCTGATATGACACA	899
Db	824	TGAGAAAGTGGCCACAATGTGTGTGTGATGGGTGGGAATTTTGGGAGCTTTAATATAGACA	883
Qy	900	TGCTCACTAGATTCGCGCGCTTTTACCCACAGAAACGGAAGAAACCATGATGATAGATCA	959
Db	884	TGCTGACTGGAGACACCCCATTTCACTGTGGGAGAAATATAAGAAACATTTGACAAATATC	943
Qy	960	TCAGGGGCAAGCTGTGACATGCCCCCTTACTACCCACCCAGATGCCCGGGACCTTGTCAAAA	1011
Db	944	TCAAAATGTAAATCAATTTTGGCTCTCCCTACCTCAACACAAAGAGAGAGATCTGCTTAAAA	1001
Qy	1020	AGTTTCTGAAACGGAAATCCAGCCAGGAGGAAATGGGGGTGGCCACAGGGGATGCTGTGATG	1077
Db	1004	AGCTGCTAAGAAAGAAATGCTGCTTCTGTCTGGGAGCTGTGCTCGGGGACGCTGGAGAAAG	1066
Qy	1080	TGCAGAGACATCCCTTTTTCGGGACATGAATTTGGGAGCATCTTGGCTGTGCGATGTGG	1133
Db	1064	TTCAAGCTCATCCATTTCTTTAGACACATTTAACTGGGAAGAACTTGTGGTCGAAAGGTGG	1122
Qy	1140	ACCCCCCTTGAAGCCCTGTGTGAGTCAGAGGAGGACGTGAGCAGATTGATACCCGCT	1199
Db	1124	AGCCCCCTTTAAACCTCTGTGTGGAATCTGAAAGGAGATGAAGTCATTTGATTTCAAGT	1188
Qy	1200	TCACACGGCAGACGCGCGGTGGACAGTCTCTGATGACACAGCCCTCAGCGAGAGTGCACAC	1255
Db	1184	TTACACGTCAGACACACTGTGTGACAGGCCAAGTATGACTCATGTCAAGTGAAGAGTGCACATC	1244
Qy	1260	AGGCTTCTCTGGGCTTCACATATGCTGGCGCGCTGTGTCTGTGGACAGCATTAAGAGGGCT	1321
Db	1244	AGGCTTCTCTGGGTTTAAATATGTGGCTCCATCTGTACTTGAAGGTGAAGAAAGT	1301
Qy	1320	TCTCTTCACGCCCAAGGTGGCTGCTACCCAGGCGCTCAACAGTAGAGCCCGGGGTCCCGC	1377
Db	1304	TTTCTCTTGAACCAAAAATCGATCAGCTCGAGAGATTTATTGGCAGGCCCAAGAACACTG	1366
Qy	1380	TCAGCCCCCTCAAGTCTCTCCCTTTTGA 1407	
Db	1364	TCAGCCCAAGTCAAAATTTTCTCTGGGGA 1391	
RESULT 9			
ABLI561			
ID ABLI561 standard; DNA; 1898 BP.			
XX	AC	ABLI561;	
XX	AC		
XX	DT	26-MAR-2002 (first entry)	
XX	DT		
XX	XX	Drosophila melanogaster genomic polynucleotide SEQ ID NO 1156.	
XX	XX		
XX	XX	Drosophila: developmental biology; cell signalling; insecticide;	
XX	XX	pharmaceutical; gene; ds.	
XX	OS	Drosophila melanogaster.	
XX	XX		
XX	XX		
XX	XX	W0200171042-A2.	

PD		27-SEP-2001.	
XX			
PF		23-MAR-2001; 2001WO-US09231.	
XX			
PR		23-MAR-2000; 2000US-191637P.	
XX			
PR		11-JUL-2000; 2000US-0614150.	
XX			
PA	(PEKE)	PE CORP NY.	
XX			
P1	Venter JC, Adams M, Li PWD, Myers EW;		
DR	WPI; 2001-656860/75.		
XX			
PT	New isolated nucleic acid detection reagent for detecting 1000 or more		
PT	genes from Drosophila and for elucidating cell signalling and cell-cell		
PT	interactions -		
XX			
PS	Claim 1; SEQ ID NO 1156; 21np + Sequence Listing; English.		
XX			
CC	The invention relates to an isolated nucleic acid detection reagent		
CC	capable of detecting 1000 or more genes from Drosophila. The invention is		
CC	useful in developmental biology and in elucidating cell signalling and		
CC	cell-cell interactions in higher eukaryotes for the development of		
CC	insecticides, therapeutics and pharmaceutical drugs. The invention		
CC	discloses genomic DNA sequences (AB161716-AB130511), expressed DNA		
CC	sequences (AB101840-AB161575) and the encoded proteins		
CC	(AB57737-AB872072).		
CC	The sequence data for this patent did not form part of the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published_pcl_sequences.		
XX			
SQ	Sequence 1898 BP; 520 A; 496 C; 496 G; 386 T; 0 other;		
	Query Match	28.3%; Score 514; DB 23; Length 1898;	
	Best Local Similarity	67.9%; Pred. No. 12; 3e-104;	
	Matches 718; Conservative 0; Mismatches 340; Indels 0; Gaps 0;		
OY	261 ACCTGACTGAGACCAAGCGTGAACGTGGGCCAGAGCCATCGGCCCATCTTTGAGC	320	
DB	176 ACCTTGCGGAGGAGATGTTAATCCAGGTAAAMTCAGCTGGAGCCCAAGACTTTGAGC	235	
OY	321 TGCTCGTGCTGTGGGCAAGGGGCGCTATGCGACAAGTGTCCAGGTGGGAAAAGGTGCAG	380	
DB	236 TCAGAAGGCTCTTGCGCAAGGTGTTATTGCCAAGCTATTTCAGGTGGCGAAGACCCTG	295	
OY	381 GCACCACTTGGGCAAAATATATGCCATGAAGTCTTAAGGAAGGCAAAATTGTGCGCA	440	
DB	296 GACGAGATGCTATAAATAATTTTGGCATGAAGAGTGCTCAAAAAGGCATTCATTGGACCA	355	
OY	441 ATGCCAAGGACACACACACACAGGGGCTGAGCGGACAATCTTAGATCAGTGAAGCAC	500	
DB	356 ATCAAAGGACACACGCGACACCCCGCGGACGGAATATCTCGAGGACAGCAAGCAATC	415	
OY	501 CCTTATATGTGAACTGGCGCTATGCTTCGCTTCAGACTGATGGGCAAACTCAACCTCATCTTG	560	
DB	416 CCTTATATAGTAGAGTAGTATTGCTTTCGACAGACAGAGGAAAACTATACCTTATACTTG	475	
OY	561 AGTGCCTCAGTGTGGCGAGCTCTTCACGCATCTGGACCGAGAGGGCATCTTCTGGAG	620	
DB	476 AATATCTCAGCGGTGAGAGGCTGTTCAATGATTTGGACGCTGAGGGCATCTTCTTAGAGG	535	
OY	621 ATAAGCGCTCGCTTACCTAGCGGTGATGATCAGCGTGGCCCTGGGCGCATGCCACTGCCAG	680	
DB	536 ATACCAACATGCTTCAATTAAGCGAAATCATTTTGGCTTGGGCCATCTACACAAATCGG	595	
OY	681 GCATCATCTACCGGGAGACCTCAAGCCCGAAGCATCATGCTCGACGACCGAGGCCACATCA	740	
DB	596 GGATCATCTACCGGATCTGGAAGCCCGAAGCATCTACTGTGATCAACAGGACAGTGA	655	
OY	741 AACTCACGACTTTTGGACTCTGCAAGAGATCTATCATATGAGGGGCCGCTACTACACT	800	
DB	656 ACTTCACGCACTTCGAGCTGTGCAAGGAGACATCAAGAGAGGTATTGTTCACCCACACT	715	

QY 801 TCTGGGACCATTTAGTACATGGCCCTGAGATTCTGGTGGGACGAGCAACCGGG 860
 DB TCTGGGACCATTTAGTACATGGCCCTGAGATTCTGGTGGGACGAGCAACCGGG 775
 QY 861 CTGTGGACCTGGTGGGACCTGGGAGCCCTGATGTACAGATCTACTGATCGCCCT 920
 DB TCTGGGACCTGGTGGGACCTGGGAGCCCTGATGTACAGATCTACTGATCGCCCT 835
 QY 921 TTACCGAGAGAACCGGAAACCATGATGATCATGAGGAGCAAGCTGGCATGC 980
 DB TCACCGAGAGAACCGGAAACCATGATGATCATGAGGAGCAAGCTGGCATGC 895
 QY 981 CCCCCCTACCTACCCAGATCCCGGACCTTGTCAAAAAGTTCTGAAACGGAATCCA 1040
 DB CAGCTTACCTACCCAGATCCCGGACCTTGTGTGCTGCTGATGTAAGCGGAGAAC 955
 QY 1041 GCCAGCGATTTGGGGGAGGAGGAGTGTCTGATGTGACAGATCATCCCTTTCC 1100
 DB CTCAGCGCTTTGGAGCGAGCCGAGATGCGGAGGCTTCAAAATACACCCATCTTCA 1015
 QY 1101 GGCACATGAATTTGGAGACCTTCTGAGCTGGCTGGACCCCTTTCAGCCCTGTC 1160
 DB AACAGCTGAATTTGGAGACCTTCTGAGCTGGCTGGACCCCTTTCAGCCCTGTC 1075
 QY 1161 TGCACTGAGAGAGAGCTGACCATTTGATACCCGCTTACACGAGAGCGGCTGG 1220
 DB TGAGAGAGAGAGAGATGTCTACAGATTCGATACAAATGATCAAGCAAAATTCAGTGG 1135
 QY 1221 ACAGTCTGATGACACACCCCTCAGCCGAGATGCCAACCAGCCCTTCTGGGCTTCAAT 1280
 DB ATTACCTGATGATGACACACCCCTCAGCCGAGATGCCAACCAGCCCTTCTGGGCTTCAAT 1195
 QY 1281 ACGTGGCGCTGTCTGTGGACAGCATCAAGAGGCG 1318
 DB ACGTGGCGCTGTCTGTGGACAGCATCAAGAGGCG 1233

RESULT 10
 AAV19873
 ID AAV19873 standard; DNA; 2556 BP.

XX AAV19873;
 XX 23-JUN-1998 (first entry)
 XX Drosophila p70S6k gene.
 DE Drosophila p70S6k gene.
 XX p70S6k; p70 S6 kinase; enzyme; kinase signalling pathway; ss.
 OS Drosophila melanogaster.
 FH Key
 FT CDS location/Qualifiers
 FT 474..2387
 FT /*tag= a
 PN W09803662-A2.
 PD 29-JAN-1998.
 PE 11-JUL-1997; 97WO-EP03680.
 XX 24-JUL-1996; 96GB-0015498.
 XX (NOVS) NOVARTIS AG.
 PA Kozma S, Stewart M, Thomas G;
 PI WPI: 1998-120783/11.
 DR P-PSDB; AAM52294.
 XX New isolated Drosophila p70 S6 kinase - is used to develop products
 PT for studying the kinase signalling pathway and for modulating the
 PT kinase activity

XX Claim 3; Page 38-42; 47pp; English.
 PS This sequence encodes the Drosophila p70 S6 kinase (p70S6) of the
 CC invention. The products are used in the study of the p70 S6 kinase
 CC enzyme. They can be used for defining the p70 S6 kinase signalling
 CC pathway and to develop agents for modulating the kinase activity. The
 CC products can also be used for the production of antibodies and for
 CC detection.
 XX Sequence 2556 BP; 717 A; 663 C; 643 G; 533 T; 0 other;

Query Match 28.3%; Score 514; DB 19; Length 2556;
 Best Local Similarity 67.9%; Pred. No. 2.5e-104;
 Matches 718; Conservative 0; Mismatches 340; Indels 0; Gaps 0;

QY 261 AGCTGACTGAGACCAAGCTGGAAGTGGCCAGAGCCGATGGGCCCCACTGCTTGAAC 320
 DB AGCTGCTGGAGAGAAATTAATCCAGGTAAATCAAGCTGGAGCCCAAGGACTTGAAC 708
 QY 321 TGCTGCTGTGGGCAAGGGGAGCTATGCGAAGGTGTCAGGTGCGAAAGTGCAAG 380
 DB TCAGAAAGTCTTGGCAAGGCGGTATGCGAAAGTATTTGAGTGGCGCAAGACCGCTG 768
 QY 769 GACGAGATGCTAACAAATATTTTGCATGAAAGTGCTCTCAAAAAGCATTCATGTGACCA 828
 DB GCACCAACTTGGGCAAAATATATGCGATGAAAGTCTTAAGAAAGCCAAATTTGTGCGCA 440
 QY 441 ATGCCAAGACACACACACAGCGGCTGAGCGGCAATTTTAAGTCAAGTGAAGCAC 500
 DB ATCAAAAGACACACACAGCGGCAACCCGCGGCAAAATATTCAGAGCAGCAAGCATC 888
 QY 501 CTTTATTTGGAACTGGCCCTATGCTTCCAGACTGAGTGGGCAAACTTACCATCATCTG 560
 DB CCTTATGTTGAGAGTATTTATGCTTCCAGACAGAGGAAATATTTATTTACTTG 948
 QY 561 AGTGGCTAGTGTGGGCGAGCTCTTACAGCATCTGAGAGCGAGAGGCAATCTTCTGGAAG 620
 DB AATATCTCAGCGGTGGAGAGGCTTATGCTTCCAGACAGAGGAAATATTTATTTACTTG 1008
 QY 621 ATACGGCTGCTTCTTACCTGCTGAGATCAGCTGGCCCTGGCCATCTCCACTCCAG 680
 DB ATACCATGCTTCTTATCTAAGCGAAATCATTTTGGCCCTGAGCATACCAAAATCG 1068
 QY 681 GCATCATCTACCGGAGCTCAAGCCGAGAAATCATGCTCAAGCCAGGCGCCACATCA 740
 DB GCATCATCTACCGGAGCTCAAGCCGAGAAATCATGCTCAAGCCAGGCGCCACATCA 1128
 QY 741 AACTGACCGACTTTGACTCTGCAAGAGTCTATCATGAGGCGCCCTCACTCACTACCT 800
 DB AGCTCAGGAGCTTTGACTCTGCAAGAGCACTATCAAGAGGCTTGTGACCCACACT 1188
 QY 801 TCTGGGCAACATTTGATGATGCGCCCTGAGATTTCTGTGGCAGTGGCCCAACCGGG 860
 DB TCTGGGCAACATTTGATGATGCGCCCTGAGATTTCTGTGGCAGTGGCCCAACCGGG 1248
 QY 861 CTGTGGACTGTGAGCCCTGGGAGCCCTGATGTACAGATGTCTACTGATGCGCCCT 920
 DB CAGTGGACTGTGAGCCCTGGGAGCCCTGATGTACAGATGTCTACTGATGCGCCCT 1308
 QY 921 TTACCGAGAGAACCGGAAACCATGATGATCATGAGGAGCAAGCTGGCATGC 980
 DB TCACCGAGAGAACCGGAAACCATGATGATCATGAGGAGCAAGCTGGCATGC 1368
 QY 981 CCCCCCTACCTACCCAGATCCCGGACCTTGTCAAAAAGTTCTGAAACGGAATCCA 1040
 DB CAGCTTACCTACCCAGATCCCGGACCTTGTGTGCTGCTGATGTAAGCGGAGAAC 1428
 QY 1041 GCCAGCGATTTGGGGGAGGAGTGTCTGATGTGAGAGATCATCCCTTTTCC 1100
 DB CTCAGCGCTTTGGAGCGAGCCGAGATGCGGCGGCTTCAAAATACCAATCTTCA 1488
 QY 1101 GGCACATGAATTTGGAGAGCACTTGTGCGCTGGCTGTGGACCCCTTTCAGGCGCTGTC 1160

DB 1489 AACACGTCACACGAGGAGTGTCTGCGACAGCCCTCCAGCCGCTATATAAACCCCTCTC 1548
QY 1161 TGCAGTCACAGGAGGAGGAGCAGTTGATACCCGCTTCACAGGAGAGCGGGTGG 1220
DB 1549 TCGAAGACGAGGATGTGTCTCACAGTTCGATACAGATTTCACAAACAAATTCACAGTGG 1608
QY 1221 ACAGTCTGATGACACAGCCCTCAGCGAGAGTCCCAACCAAGCCCTTCGCGCTTCACAT 1280
DB 1609 ATTCCCTGATGATACAAAGCCTAAGCGAAGTCCAAATTTAATTTCCAAAGTTTCACCT 1668
QY 1281 ACGTGCGCCGCTCTGTCTGCGACAGATCAAGAGAGGC 1318
DB 1669 ACGTTCACCTCGATACATGAGAGATATGCATCGGCGC 1706

RESULT 11
AAH77989
ID AAH77989 standard; DNA; 843 BP.
XX
AC AAH77989;
XX
DT 13-NOV-2001 (first entry)
DE Partial nucleotide sequence of human protein kinase SGK216.
XX
XX
KW Human; protein kinase; cancer; immune disease; cardiovascular disease;
KW brain disease; neuronal disease; Alzheimer's disease; chromosome 17;
KW Parkinson's disease; multiple sclerosis; metabolic disorder;
KW peripheral nervous system disease; amyotrophic lateral sclerosis;
KW infection; ocular disease; migraine; pain; sexual dysfunction;
KW mood disorder; attention disorder; cognition disorder; hypotension;
KW hypertension; psychotic disorder; dyskinesia; transplant rejection; ss.
XX
OS Homo sapiens.
XX
PN WO200166594-A2.
PD 13-SEP-2001.
XX
PF 02-MAR-2001; 2001WO-US066838.
XX
PR 06-MAR-2000; 2000US-0187150.
PR 29-MAR-2000; 2000US-0193404.
PR 13-NOV-2000; 2000US-0247013.
XX
PA (SUGEN-) SUGEN INC.
XX
PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
XX
DR WPI; 2001-536777/59.
DR P-PSDB; AAG67390.
XX
XX
PT Nucleic acids capable of encoding human polypeptides having a kinase or
PT kinase-like activity, useful for diagnosing a disease selected from
PT cancers, cardiovascular disease and neuronal-associated diseases (e.g.
PT Alzheimer's disease) -
XX
XX
PS Example 1; Fig 1A; 201pp; English.
XX
CC The present sequence encodes a partial human protein kinase. The
CC gene is located at chromosomal position 17q21.2-q22. The kinase
CC polypeptides are useful for diagnosing a disease or disorder
CC selected from cancers (e.g. cancers of tissues and cancers of
CC hemopoietic origin), immune-related diseases and disorders,
CC cardiovascular disease, brain or neuronal-associated diseases (e.g.
CC Alzheimer's disease, Parkinson's disease, multiple sclerosis),
CC metabolic disorders, peripheral nervous system diseases, amyotrophic
CC lateral sclerosis, viral infections, infections caused by prions,
CC infections caused by bacteria, infections caused by fungi, ocular
CC diseases, migraines, pain, sexual dysfunction, mood disorders,
CC attention disorders, cognition disorders, hypotension, hypertension,
CC psychotic disorders, dyskinesias, and organ transplant rejection.

CC Kinase inhibitors are useful for treating diseases and disorders
CC described above.
XX
SQ Sequence 843 BP; 268 A; 173 C; 187 G; 215 T; 0 other;
Query Match 25.1%; Score 455.6; DB 22; Length 843;
Best local Similarity 72.0%; Pred. No. 1.7e-91;
Matches 609; Conservative 0; Mismatches 234; Indels 3; Gaps 1;
QY 425 GCCAAATTTGTGGCAATGCAAGGACAGACACAGACAGGCGTGAAGCAATCTTA 484
DB 1 GCATGATGTAAGAAATCTTAAGATACAGCTCATACAAAGACAGATGATATTCTG 60
QY 485 GAGTCAGTAAGACCCCTTTATTTGGAAGTGGCCATTCCTTCAGACTGGGCAAA 544
DB 61 GAGGAAGTAAGGATCCCTTCATTTGATTTTAACTTATGCTTCAGACTGGTGAANA 120
QY 545 CTCTACCTCATCCTTGAGTGGCTCAGTGGTGGGAGCTTTCACAGCATGTGAGCAGAG 604
DB 121 CTCTACCTCATCCTTGAGTGGCTCAGTGGGAGGAACTATTATGCAATTAAGAAAGAG 180
QY 605 GGCATCTTCCTGGAAGATACGGGCTGCTTACCTGCGAGATACGCTGGCGCTGGGCG 664
DB 181 GGAATATTTATGGAAGACACGCTGCTTTTACTTGGCAGAAATCTCATGGCTTTGGGA 240
QY 665 CATCTCAGTCCCGAGGGCATATCTACCGGAGACCTTCAGCCGAGAAATCATATCTACAG 724
DB 241 CATTTACATCAAAAGGGATATCATATACAGAGACCTGACCGGAGAAATCATATCTTAAT 300
QY 725 AGCCAGGCGCACTCAACTGACCCGACTTTGGACTCTGCAAGAGAGTCTATCCATGAGGC 784
DB 301 CACCAAGGCTCATATGAAATACAGACTTGGACTTCGCAAGAAATCTTTCATGATGGA 360
QY 785 GCGCATCTACACACTTTCGCGGACCATTTGAGTACATGAGCCCTGAGATTCGAGGCC 844
DB 361 ACAGTACACACACATTTTGTGACAAATAGATATGATGAGCCCTGTAATCTTGAATGA 420
QY 845 AGTGGCCACAAACCGGCTGTGAGTGTGAGGCTGGGGCCCTGATGACGATGCTC 904
DB 421 AGTGGCCACAAATGCTGCTGTGAGTGTGAGGCTGGGGCAATTAATGATGACATGCTG 480
QY 905 ACTGATTCGCGCCCTTTACCGCAGAGAAACCGAAGAAACCATGATTAAGATCATCAG 964
DB 481 ACTGAGACACCCCATTTACTGGGAGAAATGAGAAACAAATTTGACAAATCATCTCAAA 540
QY 965 GGCAGCTGAGACTGCGCCCTACTACCCGAGATGCGCGGAGCTCTGCAAAAAGTTT 1024
DB 541 TGTAACTCAATTTGCTCTCTCTACCTACACAAAGAACGAGATGCTGTTAAAGCTG 600
QY 1025 CTGAAACGGAATCCAGCCAGCGGATTTGGGGTGGCCAGAGGATGCTGATGTGCAG 1084
DB 601 CTGAAAGAAATCTGCTCTCTC---TGGGAGCTGGTCTGGGAGCCTGAGAAAGTTCAA 657
QY 1085 AAGCATCCCTTTTCCGGACATGATTTGGGAGAGACTTCTGGCCCTGGGCTGTGACCCC 1144
DB 658 GCTCATCAATTTCTTTGACACATTAATCTGGGAAGCTTCTGCAAAAGGTGAGCCC 717
QY 1145 CCTTCAGGCGCTGTCTGAGTACAGAGAGAGAGTACGACATTTGATACCCGCTTCACA 1204
DB 718 CCTTTAAACCTCTGTTGCAATCTGAAGAGAGATGAAGTCAGTTTATTCGAATTTACA 777
QY 1205 CGGACAGCCCGGTGAGACATCTGATGACACAGCCCTCAGCAGAGATGCCAACAGGCC 1264
DB 778 CGTCAACACCTGTGACAGGCCAGATGACGAAATCTCAGTAAATCGCAATCGAGTTC 837
QY 1265 TTTCCTG 1270
DB 838 TTTCCTG 843

RESULT 12
AAK86891
ID AAK86891 standard; DNA; 4357 BP.

XX AAK86891;
AC
XX 07-NOV-2001 (first entry)
DT
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41703.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
PN MO200157182-A2.
PD 09-AUG-2001.
XX 17-JAN-2001; 2001WO-US01354.
PE
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 23-AUG-2000; 2000US-0227183.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.

PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 08-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244674.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 03-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.

PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI: 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX Disclosure; SEQ ID NO 41703; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
XX SQ Sequence 4357 BP; 746 A; 1337 C; 1330 G; 944 T; 0 other;

Query Match 23.2%; Score 422.2; DB 22; Length 4357;
Best Local Similarity 96.0%; Pred. No. 6.5e-84;
Matches 433; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1346 CCCAGGCGCCTCAACAGTACCCCGGAGTCCCGTCCCGCTCAAGTCTCCCTTTT 1405
DB 3900 CCTAGGAGGCTCTTATTCTGCTTGGTTTCCCTGCAAGCCCTCAAGTTCTCCCTTTT 3959
QY 1406 GAGGGGTTTCGGCCAGCCCAAGCTGCGAGAGCCCAAGAGCTACCTTACCTCCACTC 1465
DB 3960 GAGGGGTTTCGGCCAGCCCAAGCTGCGAGAGCCCAAGAGCTACCTTACCTCCACTC 4019
QY 1466 CTGCGCACCGCGCGGCTGACACCGCCCTCTCCCTTCCCTGCTCCCTTCAAGGAGC 1525
DB 4020 CTGCGCACCGCGCGGCTGACACCGCCCTCTCCCTTCCCTGCTCCCTTCAAGGAGC 4079
QY 1526 AAGAAATCCAAAGAGGCGCTGAGGCGCTAGAGAGCGGAGTGGGGTGAGGG 1585
DB 4080 AAGAAATCCAAAGAGGCGCTGAGGCGCTAGAGAGCGGAGTGGGGTGAGGG 4139
QY 1586 TAGCCCTTGAGCCCTGCTCCGCGCTGTGAGAGACAGAGACCTGAGGCAAGTTCAGA 1645
DB 4140 TAGCCCTTGAGCCCTGCTCCGCGCTGTGAGAGACAGAGACCTGAGGCAAGTTCAGA 4199
QY 1646 GACCTGGGGGTGTGTCTGGGGGTGGGGTGTGAGTGGCTATGAAGTGTGTCTGCTGGG 1705
DB 4200 GACCTGGGGGTGTGTCTGGGGGTGGGGTGTGAGTGGCTATGAAGTGTGTCTGCTGGG 4259
QY 1706 GCAGCTGTGCGCCTGATCATGGGACAGGAGGCGCGCCACACCGCGCGCTCAACTG 1765
DB 4260 GCAGCTGTGCGCCTGATCATGGGACAGGAGGCGCGCCACACCGCGCGCTCAACTG 4319

QY 1766 CTCCTGTGAAGATTAAGGCGTGAATCATG 1796
DB 4320 CTCCTGTGAAGATTAAGGCGTGAATCATG 4350

RESULT 13
AAK86892
ID AAK86892 standard; DNA: 6923 BP.
XX
XX AAK86892;
AC
XX
XX 07-NOV-2001 (first entry)
DT
XX
XX
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41704.
DE Human: immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
XX Homo sapiens.
XX
XX WO200157182-A2.
XX
XX 09-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US01354.
PF
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.

[illegible]

PR	17-NOV-2000;	2000US-0249297.
PR	17-NOV-2000;	2000US-0249299.
PR	17-NOV-2000;	2000US-0249300.
PR	01-DEC-2000;	2000US-0250160.
PR	01-DEC-2000;	2000US-0250391.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	05-DEC-2000;	2000US-0256719.
PR	06-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251868.
PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251989.
PR	11-DEC-2000;	2000US-0251990.
PR	05-JAN-2001;	2001US-0254097.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
DR	WPI: 2001-483426/52.	
XX		
PT	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,	
PR	useful for preventing, diagnosing and/or treating cancers and	
PT	metastasis -	
PS	Disclosure; SEQ ID NO 41704; 3071bp + Sequence Listing; English.	
XX		
CC	AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)	
CC	amino acid sequences given in AAM62170 to AAM91921. (I) have cytostatic	
CC	activity, and can be used in gene therapy and vaccine production. (I)	
CC	treatments and polynucleotides may be used in the prevention, diagnosis and	
CC	treatment of diseases associated with inappropriate (I) expression. For	
CC	example, they may be used to treat disorders associated with decreased	
CC	expression by rectifying mutations or deletions in a patient's genome	
CC	that affect the activity of (I) by expressing inactive proteins or to	
CC	supplement the patients own production of (I). Additionally, (I)	
CC	polynucleotides may be used to produce the secreted (I), by inserting	
CC	the nucleic acids into a host cell and culturing the cell to express the	
CC	protein. (I) proteins and polynucleotides may be used to prevent,	
CC	dialnose and treat immune/hematopoletic-related diseases, especially	
CC	cancers and cancer metastases of hematopoletic-derived cells. AAK64703	
CC	to AAK87694 represent human immune/hematopoletic antigen genomic	
CC	sequences from the present invention. AAK54942 to AAK54950 and AAM62169	
CC	represent sequences used in the exemplification of the present invention.	
XX		
SQ	Sequence 6923 BP; 1252 A; 2025 C; 2044 G; 1602 T; 0 other:	
	Query Match	23.2%; Score 422.2; DB 22; Length 6923;
	Best Local Similarity	96.0%; Pred. No. 7.3e-84;
	Matches 433; Conservative	0; Mismatches 10; Indels 0; Gaps 0;
QY	1346 CCCAGGCGCCTCAACAGTAGCCCCGGGTGCCCGTCAGGCCCCCTCAAGTCTCCCTTTT	1405
DB	6466 CTAGAGGAGCTCTATTCTTGCTTGCTTGCTTGCCTCGAGGCCCTCAAGTCTCCCTTTT	6525
QY	1406 GAGGGGTTTTGGGCCCAAGCCCAGACTGCGCGGAGCCACGAGGACTTACTTCTCATCTC	1465
DB	6526 GAGGGGTTTTGGGCCCAAGCCCAGACTGCGCGGAGCCACGAGGACTTACTTCTCATCTC	6585
QY	1466 CTAGCACGCGCGCGCGCTTCGACACACGCGCCCTTCATCGCGTCCCGCCCTCAGGAGCC	1525
DB	6586 CTAGCACGCGCGCGCGCTTCGACACACGCGCCCTTCATCGCGTCCCGCCCTCAGGAGCC	6645
QY	1526 AAGAAGTCCAAGAGGGGCGCTGGGGCTCCACGAGCGCTAGGAAGCCGGGTGGGGGTGAGGG	1585
DB	6646 AAGAAGTCCAAGAGGGGCGCTGGGGCTCCACGAGCGCTAGGAAGCCGGGTGGGGGTGAGGG	6705
QY	1586 TAGCCCTTAGCCCTGTCTCCCTCGGGCTGTGAAGACAGACAGAACCTTGGGCCAGTTCCAGA	1645
DB	6706 TAGCCCTTAGCCCTGTCTCCCTCGGGCTGTGAAGACAGACAGAACCTTGGGCCAGTTCCAGA	6765

QY 1646 GACCTGGGGGTGTCTGTGGGGGTGGGCTGTGACTGCTATGAAAGTGTGTCTGTCTGGG 1705
|||||
DB 6766 GACCTGGGGGTGTCTGTGGGGGTGGGCTGTGAGTGTGAAGTGTGTCTGTCTGGGG 6825
QY 1706 GCAGCTGTGCCCCGTAATCATGAGGACGAGAGGGGCCCCGACACCCCGCGCTCACTG 1765
|||||
DB 6826 GCAGCTGTGCCCCGTAATCATGAGGACGAGAGGGGCCCCGACACCCCGCGCTCACTG 6885
QY 1766 CTCCTCGTGAAGATTTAAAGGGCTGAATCATG 1796
|||||
DB 6886 CTCCTCGTGAAGATTTAAAGGGCTGAATCATG 6916

RESULT 14
ABK64273
ID ABK64273 standard; DNA: 445 BP.
XX
AC ABK64273:
XX
DT 18-JUN-2002 (first entry)
XX
DE Human benign prostatic hyperplasia gene #168.
XX
KM Human: benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
XX
OS Homo sapiens.
XX
PN MO200212440-A2.
XX
PD 14-FEB-2002.
XX
PE 07-AUG-2001; 2001WO-US24708.
XX
PF 07-AUG-2000; 2000US-223323P.
XX
PR 05-JUN-2001; 2001US-0873319.
XX
PA (GENE-) GENE LOGIC INC.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
PI Mungner WE, Kuikarni P, Getzenberg RH, Waga I, Yamamoto J;
XX
DR WPI; 2002-257476/30.
XX
PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PT detecting expression levels of one or more genes in prostate cells from
PT patient that are differentially regulated compared to normal prostate
XX
XX
PS Disclosure: Page 131; 444bp; English.
XX
XX The invention relates to a method of diagnosing (I) the onset or
CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
CC or identifying an agent that modulates the onset or progression of BPH.
CC The method is based on changes in gene expression in BPH tissue isolated
CC from patients exhibiting different clinical states of prostate
CC hyperplasia as compared to normal prostate tissue. (I) comprises
CC detecting the expression levels of one or more genes in prostate cells
CC from the subject that are differentially regulated compared to normal
CC prostate cells. (II) comprises preparing a first gene expression profile
CC of BPH cells or BPH-like cell population, exposing the cells to the
CC agent, preparing a second gene expression profile of the agent exposed
CC cells, and comparing the first and second gene expression profiles.
CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
CC useful for identifying an agent that modulates the onset or progression
CC of BPH. The methods are useful to present information identifying
CC the expression level in a tissue or cells, by comparing the expression
CC level of genes given in the specification in the tissue or cells to the
CC level of expression of gene in the database, and displaying the
CC expression levels of at least one gene in the tissue or cell sample
CC compared to the expression level in BPH. Agents using (II) are useful for
CC treating BPH or prostate cancer. ABK64106-ABK64860 represent human
CC benign prostatic hyperplasia gene sequences of the invention.
XX

SO Sequence 445 BP; 72 A; 163 C; 125 G; 85 T; 0 other;
Query Match 23.1%; Score 418.8; DB 24; Length 445;
Best Local Similarity 99.1%; Pred. No. 2e-83;
Matches 442; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1043 CAGCGGATTTGGGGGTGGCCCCAGGGGATGCTGCTGATGTGCAAGACATCCCTTTTCCGG 1102
|||||
DB 2 CAGCGGATTTGGGGGTGG-CCAGGGGATGCTGCTGATGTGCAAGACATCCCTTTTCCGG 60
QY 1103 CACATGAATTTGGGACGACCTTCTGGCCCTGGCGTGTGAGACCCCTTTACAGCCCTGTCTG 1162
|||||
DB 61 CACATGAATTTGGGACGACCTTCTGGCCCTGGCGTGTGAG-CCCCCTTTACAGCCCTGTCTG 119
QY 1163 CAGTCAGAGGAGGACGTCGACCCAGTTTGATACCCGCTTTCACAGGCGACAGCCGATGGAC 1222
|||||
DB 120 CAGTCGAGGAGGACGTCGACCCAGTTTGATACCCGCTTTCACAGGCGAGAGCCGATGGAC 179
QY 1223 AGTCCTGATGACACAGCCCTTCAGCGAGAGTGCACACAGGCGCTTCTGGGCTTTCATATAC 1282
|||||
DB 180 AGTCCTGATGACACAGCCCTTCAGCGAGAGTGCACACAGGCGCTTCTGGGCTTTCATATAC 239
QY 1283 GTGGCGCCGTCGTGTCGAGACGATCAAGAGAGGGGCTTTCCTTCCAGGCCAAGCTGGCG 1342
|||||
DB 240 GTGGCGCCGTCGTGTCGAGACGATCAAGAGAGGGGCTTTCCTTCCAGGCCAAGCTGGCG 239
QY 1343 TCACCCAGGCGCCTCAACAGTAGCCCCCGGGTCCGCTACGCCCCCTCAAGTTCTCCCT 1402
|||||
DB 300 TCACCCAGGCGCCTCAACAGTAGCCCCCGGGTCCGCTACGCCCCCTCAAGTTCTCCCT 359
QY 1403 TTTGAGGGGTTTGGGCCACCCCGAGCTGCGGAGGCCAGGAGCTACTTACTCCCA 1462
|||||
DB 360 TTTGAGGGGTTTGGGCCACCCCGAGCTGCGGAGGCCAGGAGCTACTTACTCCCA 419
QY 1463 CTCCTGCCACCGCGCGCGCCCTCGAC 1488
|||||
DB 420 CTCCTGCCACCGCGCGCGCCCTCGAC 445

RESULT 15
AAF15983
ID AAF15983 standard; cDNA: 673 BP.
XX
AC AAF15983:
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen nucleotide sequence SRO ID NO:418.
XX
XX Human: prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnary; gastrointestinal; nephrotoxic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease; ss.
XX
XX Homo sapiens.
OS
PN MO200055174-A1.
XX
PD 21-SEP-2000.
XX
PE 08-MAR-2000; 2000WO-US05988.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
PI Rosen CA, Ruben SM;
XX
XX WPI; 2000-587513/55.
DR P-PSDB; AAB56780.
DR

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 18, 2002, 20:57:05 ; Search time 2070 Seconds

(without alignments)
3872.834 Million cell updates/sec

Title: US-09-762-258-2

Perfect score: 2614

Sequence: 1 MARGRRAGGAAAMAVFDL.....PIRPPSGTKSKRGGRGRGR 495

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 segs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Command line parameters:
-MODEL=frame_plus_p2n.model -DEV=xlh
-O=/cgn2.1/USPTO_SPOOL/US09762258/runat_13112002.102448.5072/app_query.fasta_1.647
-DB=EST -QFMT=fastap -SUFFIX=1st -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blousum62 -TRANS=human4.0.cdi -LIST=45
-LOCALALIGN=200 -THR.SCORE=DCT -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=us09762258_accn_1.1.763 @runat_13112002.102448.5072 -NCPU=6 -ICPU=3
-NO_XLPTX -NO_MMAP -LARGEQUENT -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -Delop=6 -Delext=7

Database :
EST :
1: em_estba :
2: em_estchum :
3: em_estlin :
4: em_estlmu :
5: em_estlov :
6: em_estpl :
7: em_estro :
8: em_hlc :
9: gb_est1 :
10: gb_est2 :
11: gb_hlc :
12: gb_est3 :
13: gb_est4 :
14: gb_est5 :
15: em_estfun :
16: em_estom :
17: gb_gss :
18: em_gss_hum :
19: em_gss_inv :
20: em_gss_pin :
21: em_gss_vrt :
22: em_gss_fun :
23: em_gss_mam :
24: em_gss_mus :
25: em_gss_other :
26: em_gss_pro :
27: em_gss_rtd :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2391.5	91.5	1834	11	AK014412	AK014412 Mus muscu
2	1648.5	63.1	992	9	AL529444	AL529444 AL529444
3	1574	1574	1037	14	BM923000	BM923000 AGENCOURT
4	1569.5	60.0	1037	14	BM059474	BM059474 AGENCOURT
5	1543.5	59.0	1014	14	BM052654	BM052654 AGENCOURT
6	1541.5	59.0	1005	13	BM423942	BM423942 AGENCOURT
7	1511.5	57.8	943	14	BM643418	BM643418 AGENCOURT
8	1493.5	57.1	1075	14	BM062171	BM062171 AGENCOURT
9	1481	56.7	952	14	BM918927	BM918927 AGENCOURT
10	1477	56.5	1048	14	BM642404	BM642404 AGENCOURT
11	1477	56.5	1048	14	BM052262	BM052262 AGENCOURT
12	1454	55.6	849	9	AL527983	AL527983 AL527983
13	1448.5	55.4	923	14	BM890823	BM890823 AGENCOURT
14	1426	54.6	1176	14	BM061526	BM061526 AGENCOURT
15	1422.5	54.4	1049	14	BM054269	BM054269 AGENCOURT
16	1421.5	54.4	1018	14	BM057747	BM057747 AGENCOURT
17	1408.5	53.9	1080	14	BM062488	BM062488 AGENCOURT
18	1387	53.1	834	12	BM792760	BM792760 601584616
19	1387	53.1	895	9	AL521570	AL521570 AL521570
20	1376.5	52.7	1044	14	BM072582	BM072582 AGENCOURT
21	1353.5	51.8	883	14	BM877063	BM877063 AGENCOURT
22	1351.5	51.7	997	14	BM048653	BM048653 AGENCOURT
23	1333	51.0	854	14	BM0431606	BM0431606 AGENCOURT
24	1331	50.9	891	12	BM829030	BM829030 602753356
25	1328	50.8	850	9	AL560524	AL560524 AL560524
26	1325	50.7	793	13	BM907389	BM907389 603063732
27	1324.5	50.7	789	9	AL525066	AL525066 AL525066
28	1323.5	50.6	867	13	BM121158	BM121158 603035053
29	1318.5	50.4	865	12	BM792968	BM792968 601585633
30	1318.5	50.4	764	12	BM673589	BM673589 602661825
31	1312	50.2	1109	14	BM058742	BM058742 AGENCOURT
32	1306	50.0	1082	13	BM561338	BM561338 AGENCOURT
33	1301	49.8	757	13	BM1084346	BM1084346 602689663
34	1299	49.7	767	9	AL519476	AL519476 AL519476
35	1288	49.3	858	14	BM0961675	BM0961675 AGENCOURT
36	1287	49.2	899	14	BM0942698	BM0942698 AGENCOURT
37	1285	49.2	783	13	BM825778	BM825778 603072188
38	1281	49.0	814	12	BM488888	BM488888 602534889
39	1265.5	48.4	2957	11	AK012045	AK012045 Mus muscu
40	1264.5	48.4	1057	14	BM915476	BM915476 AGENCOURT
41	1254	48.0	757	13	BM020218	BM020218 603648807
42	1251.5	47.9	842	12	BM797272	BM797272 601587631
43	1230	47.1	780	13	BM224008	BM224008 602942692
44	1226	46.9	896	12	BM799643	BM799643 601592525
45	1226	46.9	1152	14	BM052906	BM052906 AGENCOURT

ALIGNMENTS

RESULT 1
AK014412
LOCUS
DEFINITION
AK014412 1834 bp mRNA linear HMC 19-JAN-2002
Mus musculus 18 days pregnant adult female placenta and extra
embryonic tissue cDNA, RIKEN full-length enriched library,
clone:3830402N06;protein tyrosine phosphatase, receptor type, C
polypeptide-associated protein, full insert sequence.
ACCESSION
AK014412
VERSION
AK014412.1 GI:12852247
KEYWORDS
HMC; CAP trapper.
SOURCE
Mus musculus (strain: C57BL/6J) 18 days pregnant adult female
placenta and extra embryonic tissue cDNA to mRNA, clone:lib:RIKEN
full-length enriched mouse cDNA library clone:3830402N06.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, N., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuno, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexed sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aikawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanka, I., Saito, T., Okazaki, Y., Gotoori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Futschmann, M., Gaasterland, T., Gissi, C., King, B., Kochiya, H., Kusl, P., Lewis, S., Matsuno, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Stabili, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hotmann, M., Hume, D. A., Kamiyama, Lee, N. H., Lyons, P., Machomoni, L., Mashima, J., Mazzarelli, J., Mombere, P., Nordone, P., Rling, B., Ringwald, C., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyo-Oka, K., Wang, K. H., Wetz, C., Whiteker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S. and Hayashizaki, Y.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217851
REFERENCE	5 (bases 1 to 1834)
AUTHORS	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arikawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hangaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imocani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Nunakata, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Saeki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toyata, T., Yamamura, T., Yamanka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gc.riken.go.jp).

URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAAGAAATCCACGAGCCTCTTTTGTTCCTTCA 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 50.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAAGAAATTCGAGTTAATAATTATCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

```

FEATURES
Source
    Location/Qualifiers
        1..1834
            /organism="Mus musculus"
            /strain="C57BL/6J"
            /db_xref="FANTOM.DB:383040ZNO6"
            /db_xref="MGD:MGI:1903117"
            /db_xref="taxon:10090"
            /clone="383040ZNO6"
            /sex="female"
            /tissue-type="placenta and extra embryonic tissue"
            /clone.lib="RIKEN full-length enriched mouse cDNA library"
            /dev_stage="18 days pregnant adult"
        1..1834
            /gene="Ptpcrap"
            80..1537
                /gene="Ptpcrap"
                /note="data source:MGD, source key:MGI:97811, evidence:ISS protein tyrosine phosphatase, receptor type, C polypeptide-associated protein putative"
                /codon_start=1
                /protein_id="BAB29335.1"
                /db_xref="GI:12852248"
                /db_xref="MGD:MGI:97811"
                /translation="MAAVFDLDETEGSGSEGEPEPSPADVCPGLGRNAGLETYGH YEVELETSVVNLGPERRIGPHCELLSVLKGGGVQVRKYVGYNLGRITAKRYLR KAKIVCSADKTAFRAERINILLESVKHPFIYELAYAFQTGKLYLIIECLSGEGLFTHL ERBEIFLEDPAECFLAEITLTALGHSGLIIRDLKPENIMLSOGHIIKLTFGLCKE SIHGGAITHTHECGITEYMAPELLVRTGNHRNAVDMWSIALMYMLNGSPPTENRKK TMOKIRTKGLVPRLPGYTELPDARDLAKRTKLKNPPORISGGIDGADADVGRHFRRIND DLARARYDPFRPSLQSIEDVVSOFDAFTKOTPDVSDPDOTALSESANQALGFITYAP SVLDSTIEGFSFQPKLRNSPRLNSSPTIPSLKFSPFEGRFPSGPPEMEPSLPLP LPSPSPPTSTAFLPIRPSPSGTRKSKKGGRGRSGR"
BASE COUNT      432 a          527 c          512 g          363 t
ORIGIN
Alignment Scores:
Pred. No.:       1,24e-186           Length:         1834
Score:           2391.50             Matches:         454
Percent Similarity: 94.55%           Conservative:     14
Best Local Similarity: 91.72%         Mismatches:      24
Query Match:      91.49%             Indels:          3
DB:               11                 Gaps:            1
US-09-762-258-2 (1-495) x AK014412 (1-1834)
Oy      4 Glytargatgalaatvgglyalaglyalaaahetataaavaipheaspleuaspleuglu 23
Db      50 GCCAAGAGGCTCCGCCGACCGCGGGCCCATGCGCGCCGATTTGATTTGACTTGAG 109
Oy      24 Ttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt 43
Db      110 ACCGAGGAAGGAGGAGCGAGGCGGAGGCGAACCGGAGTTCAACCCTCGCGAGAGCTGTGCC 169

```

QY 44 LeuAlaGluLeuArgAlaAlaGlyLeuGluProValGlyHisTyrGluGluValGluLeu 63
 DB 170 CTGGCGCAATTAAAGGCGCTGCTGCGTGGAGACAGTGGACATATGACAGAGTAGAGCTG 229
 QY 64 ThrGluThrSerValAsnValGlyProGluArgGlyGlyProHisCysPheGluLeu 83
 DB 230 ACAGAGACAGCGGTGAACCTGGCTCTGAGCGCATCGGCGCCACAGCTGTTGAGGCTACTG 289
 QY 84 ArgValLeuGlyGlyGlyGlyTyrGlyValPheGluValArgGlyValGlnGlyThr 103
 DB 290 AGCTGACGGGGAGAGGGGGCTATGGCAGGCTGTCACAGTGAAGAAAGTGAAGGACAC 349
 QY 104 AsnLeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAla 123
 DB 350 AACTGGGAAAAATATATGCCATGAAGGCTTTAAGGAGGCCAGATTATATGACAGTGC 409
 QY 124 LysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPhe 143
 DB 410 AAGGACACAGCCCATACCCGGGCTGAGAGAACATCTGAAATCTGTGAAGCATCCCTTC 469
 QY 144 IleValGluLeuAlaTyrAlaPheGlnThrGlyGlyLysLeuTyrIleuLeuGlyCys 163
 DB 470 ATTGTAGAAGCTGCGCTATGCTTCCAGACAGGTGGCAAACTGCTACCTCATCCCTGGAGTGC 529
 QY 164 LeuSerGlyGlyGluLeuPheThrHisLeuGluArgGlyLysIlePheLeuGluAspThr 183
 DB 530 CTCATGCTGGGTGAGCTCTTCACACATCTTGAGCGAGAAAGCATCTCTCGAGACACAA 589
 QY 184 AlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyLe 203
 DB 590 GGCTGCTCTACCTGGCAGAGATCAACACTAGCCCTGGCCATCTCCATCCACGGGCATC 649
 QY 204 IleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeu 223
 DB 650 ATCTACCCGGGACCTCAAGCCTGAGAACATCATGCTCAGCAGCGGCCACATCAAACTG 709
 QY 224 ThrAspPheGlyLeuCysLysGluSerIleHisGlyAlaValHisThrHisThrPheCys 243
 DB 710 ACGACCTTGGACTTGGCAGAGATCCATTCATGAGGGTGTCTATCATCACTCATCTCTGT 769
 QY 244 GlyThrIleGlyLysMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaVal 263
 DB 770 GGCACCATGAGTACATGAGCCCGCAGAGATTTAGTCCGACATGTCACAAACCGGCGAGTG 829
 QY 264 AspTyrTrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThr 283
 DB 830 GACTGTGTGAGCTGGAGACCTGTGATGTACGACATGCTCATGATCGCCGCTTCACT 889
 QY 284 AlaGluAsnArgLysLysThrMetLysPheIleArgGlyLysAlaLeuProPro 303
 DB 890 GGAGGAAACCGGAGAAACCTATGATTAATTAAGGAAAGCTGTGCTGCCCCC 949
 QY 304 TyrLeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGln 323
 DB 950 TACCTCAACCCCGGATGCCGGGACCTTGCCAAAAGTTCTGAAGGGAGAACCCCACTCAG 1009
 QY 324 ArgIleGlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHis 343
 DB 1010 CCAATTGGGGGTGGCTGGAGATGCTCTGATGTCCAGAGGACCCCTTTTCCGGCAC 1069
 QY 344 MetAsnTrpAspLeuLeuAlaTrpArgValAspProProPheArgProCysLeuGln 363
 DB 1070 ATCAATTTGGATATCTTTGGCCCGCGGTGGACCTCTCCCTGCGGCAAGTGGCAA 1129
 QY 364 SerGluGluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSer 383
 DB 1130 TCAGAAAGAGATGTGAGCAGTTTGTATGACGATTCACACGGGAGACGCCGGTAGTACT 1189
 QY 384 ProAspAspThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTyrVal 403
 DB 1190 CCAGATGACACAGCCCTCAGTGTAGAGTGCACCAACCAAGCCCTCTGGGCTTACATATGTG 1249

QY 404 AlaProSerValLeuAspSerIleLysGluGlyPheSerPheGlnProLysLeuArgSer 423
 DB 1250 GCACCTTGTCTCTGGACAGCATCAAGAGGGCTTCTCTTCAGGCCAAGCTGCTTCT 1309
 QY 424 ProArgArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerProPhe 443
 DB 1310 CCCAGACGCGCTTAACAGCAGTCCCGCCACCCCATCAGCCCTCAAGTTCTCTCCCTTT 1369
 QY 444 GluGlyPheArgProSerProSerLeuProGluProThrGluLeuProProLeu 463
 DB 1370 GAGGGGTTCGGCCCAAGTCCCGCCGACCAAGAGCCCATGAGCCATCTTACCTCCACTC 1429
 QY 464 Leu-----ProProProProProSerThrAlaProLeuProIleArgProPro 480
 DB 1430 CTCACCATCACACACATCACACACACACACACACACACACACACACACACACACAC 1489
 QY 481 SerGlyThrLysLysSerLysArgGlyArgGlyArgProGlyArg 495
 DB 1490 TCAGAACCAAGAACATCAAGAGGAGCGGCGCTCAGGCGT 1534
 RESULT 2
 AL529444
 LOCUS AL529444 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD006YE23 5
 DEFINITION prime, mRNA sequence.
 ACCESSION AL529444
 VERSION AL529444.1 GI:12792937
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 992)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES
 source
 1..992
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DD006YE23"
 /clone_lib="LTI_NFL001_NBC4"
 /sex="male"
 /tissue_type="neuroblastoma cells"
 /lab_host="PH10B"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library of the pCMVSPORT 6 by life technologies. Contact : Peng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : liliang@life.com URL : http://fulllength.invitrogen.com"
 BASE COUNT 220 a 278 c 306 g 184 t 4 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 8.75e-126 Length: 992
 Score: 1648.50 Matches: 320
 Percent Similarity: 97.87% Conservative: 2
 Best Local Similarity: 97.26% Mismatches: 6
 Query Match: 63.06% Indels: 1
 DB: 9 Gaps: 1
 US-09-762-258-2 (1-495) x AL529444 (1-992)
 QY 8 ArgGlyAlaGlyAlaAlaMetAlaAlaValPheAspLeuAspLeuGluThrGluGluGly 27

Db	5	CGGGC-----GGGGCCCATGGCGCGCTGTTTGA	TTTTTGGATTGTGGATTGTGGAAACGAGGAAGC	61
Oy	28	SerGIuGIyGIuGIyGIuProGIuSerProAlaAspAlaCysProLeuAlaGIuLeu		47
Db	62	AGCGAGGCGAGGGGAGCAGAGCTCAGCCCGGGGAGCGATGTTCCCTTGCCGAGTTG	TTTTT	121
Oy	48	ArgAlaAlaGIyLeuGIuProValGIyHisTrpGIuGIyValGIuLeuThrGIuThrSer		67
Db	122	AGGCGAGCTGGCGCTAGACCTGTGGGACACTGTGAAGAGGTGGAGCTACTGAGACCAAC		181
Oy	68	ValAsnValGIyProGIuArgTLeGIyProHisCysPheGIuLeuLeuArgValLeuGIy		87
Db	182	GTGAACGTTGGCGCCAGAGCGCATCGGGCCCACTGCTTGAAGCTGCTCGTGTGCTGGGC		241
Oy	88	LysGIyGIyTrpGIyLysValPheGIuValArgLysValGIyTrpHisAspLeuGIyLys		107
Db	242	AAAGGGGGCTATGGGAAGGTGTCCAGGTGGCAAAAGGTGCAAGGACCAACACTTGGGCAAA	TTTTT	301
Oy	108	ILeuTrAlaMeLysValLeuArgLysAlaLysIleValArgAsnAlaLysAspThrAla		127
Db	302	ATATATGCCATGAAGAGTCTTAAGGAAGCCAAATATGTGGCCMAATGCCAAGAGACACACA		361
Oy	128	HisTrpArgAlaGIuArgAsnIleLeuGIuSerValLysHisIleProPheIleValGIuLeu		147
Db	362	CACACACGGGCTGAGCGGAGAACATTTCTAAGTCAGTTAAGCAACCCCTTATTTGTGAATCG		421
Oy	148	AlaTrpAlaPheGIuThrGIyLysLeuTrpLeuIleLeuGIuLysLeuSerGIyGIy		167
Db	422	GCGTATGGCTTCCAGACCTCGGTGGCAAACTTCAACCTCACTTGAAGTTCTCTAGTGTGGC	TTTTT	481
Oy	168	GIuLeuPheTrpHisLeuGIuArgGIuGIyIlePheLeuGIuAspThrAlaCysPheTrp		187
Db	482	GAGCTCTTCAGCACTCGAGGAGAGGGGCACTTCCGGAAGATACGGCTGCTTCTAC		541
Oy	188	LeuAlaGIuIleThrLeuAlaLeuGIyHisLeuHisSerGIyGIyIleIleTrpArgAsp		207
Db	542	CTGGCTGGAGATCAGCGTGGCCCTGGGCCATCTCCACTCCAGGGCATATCTACCGGGAC		601
Oy	208	LeuLysProGIuAsnIleMetLeuSerSerGIyGIyHisIleLysLeuThrAspPheGIy		227
Db	602	CTCAAGCCCGGAACATCATGCTCTCGAGCCAGGCGCCACATCAACATGACCGACTTTGA		661
Oy	228	LeuCysLysGIuSerIleHisGIuGIyAlaValIleTrpHisTrpPheCysGIyThrIleGIu		247
Db	662	CTCTCGAAGGAGTCTATCATGAGGGGCCCGCTACATCCACACTTCTTGGGGACCAATTAG	TTTTT	721
Oy	248	TyrMetAlaProGIuIleLeuValArgSerGIyHisAsnArgAlaValAspTrpTrpSer		267
Db	722	TACATGGCCCTCGAGATTTCTGGTGGCAGTGGCCACACCGGGCGTGTGGACTGTGGAGGC		781
Oy	268	LeuGIyAlaLeuMetTrpAspMetLeuThrGIySerProProPheTrpAlaGIuAsnArg		287
Db	782	CTGGGGGCGCTGATGTACAGACATGCTCACTGGATCGCGCCCTTACCGCAGAGAACGG		841
Oy	288	LysLysTrpMetAspLysIleIleLeuGIyLysLeuAlaLeuProProTyrLeuThrPro		307
Db	842	AAAGAAACCATGTGATTAATCATCAGGGGCAAGCTGGGACTGCCCCCTTACTTACCCCCA	TTTTT	901
Oy	308	AspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGIuArgTLeGIyGIy		327
Db	902	GAMGGCCCGGAGCACTGTGAHAAAGATTTCTGAAGACGATCCAGAGMACCGATTTGGGGG	TTTTT	361
Oy	328	GIyProGIyAspAlaAlaAspValGIu		336
Db	962	TGGCCAGGGGAGTGTGTGAAGTCA	988	
RESULT 3				
LOCUS	BM923000	1076 bp	mRNA	linear
DEFINITION	ACGNCCURT_6632221 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5756950			
ACCESSION	BM923000			

VERSION	BM923000.1 GI:19373379						
KEYWORDS	EST.						
SOURCE	human.						
ORGANISM	<i>Homo sapiens</i>						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.						
AUTHORS	1 (bases 1 to 1076)						
TITLE	NIH-MGC http://mgc.nci.nih.gov/						
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)						
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cga@rsf-mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAMA2798 row: f column: 23 High quality sequence stop: 670.						
FEATURES	Location/Qualifiers						
SOURCE	1..1076						
	/organism="Homo sapiens"						
	/db_xref="taxon:9606"						
	/clone="IMAGE:5756950"						
	/clone_1lb="NIH_MGC_118"						
	/tissue_type="leukocyte"						
	/lab_host="DH10B"						
	/note="Vector: PCMV-SPORE6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research genetics tracking code 027. Note this is a NIH-MGC Library."						
BASE COUNT	229	a	313	c	333	g	198 t
ORIGIN	3 others						
Alignment Scores:							
Pred. No.:	1,3e+119				length:	1076	
Percent Similarity:	1574.00				Matches:	315	
Best Local Similarity:	92.77%				Conservative:	6	
Query Match:	91.04%				Mismatches:	18	
DB:	60.21%				Indels:	7	
	14				Gaps:	3	
US-09-762-258-2 (1-495) x BM923000 (1-1076)							
OY	4	GLYARGALAAAGLIALAIAALMETALAIAVALPHEASPLEUASPLEUGLU	23				
DB	44	GGCGACGCGGCCCGGGGCGCCGCCGCATGGCGCGCTGTTCATTGGATTGGAG	103				
OY	24	ThrgluglugsrgrgluglulgugluvgluProglubenseerProlaasplacyspro	43				
DB	104	ACGGAGAAGCACGAGGGGCGAGGCGACCACAGACTCAGCCCCCGGAGCAGTGTCCC	163				
OY	44	LeuaiaagluenuaAgalaalagluelugluProvalaGlYhiistrigluLuvaiglueu	63				
DB	164	CTTGCGCGATTGAAGGCAAGCGGGCGCTAGACCTGTGGACAATAAGAGGTGAGCTG	223				
OY	64	ThrluglrserValanavalglyProgluarllleglyProhlscysPheglueuenu	83				
DB	224	ACTGAGACACGTAACGTTGGCCAGACGCATCGGGGCCACACGCTTTAGAGCTGCG	283				
OY	84	ArgVallauglylsygsylgyTYRGLYLysVaLPhcglNValArqylsyValglnslYThr	103				
DB	284	CCTGTGCTGGGCAAGGGGGGCTATGCGCAAGGTGTTCCAGGTGCGAAGGTGCAAGGCAC	343				
OY	104	AsnleuglylsileTyrrAlaMeLlysValleuArqLYsAlaLyAlaYlleValArqAnaLa	123				

Db 344 AACTGGGCAAAATATATGCCATGAAAGTCTTAAGGAAGCCAAATTGTGGCAATGCC 403
QY 124 LysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValIysHisProPhe 143
Db 404 AAGGACACACACACACACGCGCTGAGCGGAACATCTTAAGTACGAGGAAGCACCCCTTT 463
QY 144 ILevalGluLeuAlaTyrAlaPheGlnThrGlyIleGlyLeuTyrIleLeuGluCys 163
Db 464 ATGTGGAACTGGCCTATGCTTCACAGACGTGGGCAAACTACCTACCTCATCTTGAAGTGC 523
QY 164 LeuSerGlyGlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThr 183
Db 524 CTCAGGTGGGCGAGCTCTTCAGCATCTTGAGAGGAGGAGCATCTCCGGAAGATACG 583
QY 184 AlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIle 203
Db 584 GCTGCTCTACCTGGCTGAGTACGCTGGCCCTGGGCCATCTCCACCTCCAGGGATC 643
QY 204 IleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeu 223
Db 644 ATCTACGGGACCTCAAGCCCGAAGACATCATGCTCAGACGAGGCCACATCAAACTG 703
QY 224 ThrAspPheGlyLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCys 243
Db 704 ACCGACTTTGGACTCTGCAAGGAGTCTATCATGAGGCGCCGCTCACACTCTCTG 763
QY 244 GlyThrIleGluTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaVal 263
Db 764 GGACACATTGATGATAGCGCCCTGAGATCTGCTGGCGGACCAACCGGCGTGG 823
QY 264 AspTyrTrpSerLeuGlyAla-LeuMetTyrAspMetLeuThrGlySerProPheThr 283
Db 824 GACTGGTGGAGCTGGGGGCGCCCTGATGTCACACATGCTACAGTGCAGCGCCCTTTCA 883
QY 283 rAlaGluAsnArgLysLysThrMetAspLysIleIleArgLysLeu--AlaLeuPr 302
Db 884 CCGAGAGAACCGGAAACACCTGTGATAGATCTCCGGGCAAGGCTGGAGTGC 943
QY 302 oProTyrLeuThrProAspAlaArgAspLeu-ValIysLysPheLeuLysArg--AsnPr 321
Db 944 CCTACCTCAACCCAGATGCCCCCGGACCTTGTCAAAAAGTTTGTAAAGGATCCAC 1003
QY 321 roSerGlnArgIleGlyGlyIleProGlyAspAla-----AlaAspValGlnArgHis 338
Db 1004 CCNNGGGAATTTGGGGGGGGGCGCCCGGGAATCTCTCTGAAAGGCAAAAAAACTTC 1063
QY 339 ProPhePheArg 342
Db 1064 CCTTTTTCGCG 1075

RESULT 4
LOCUS BQ059474 1037 bp mRNA linear EST 29-MAR-2002
DEFINITION AGENCOURT_7050085 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5815533
5', mRNA sequence.
ACCESSION BQ059474
VERSION BQ059474.1 GI:19818814
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1037)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LNCM2070 row: 0 column: 22
High quality sequence stop: 611.
Location/Qualifiers
1. 1037
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5815533"
/clone_lib="NIH-MGC-99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Lymph. Vector: pOT87. Site 1: XhoI. Site 2:
EcoRI. cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGACAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the Laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH-MGC
Library."

BASE COUNT 206 a 356 c 282 g 191 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 2, 92e-119 Length: 1037
Score: 1569.50 Matches: 307
Percent Similarity: 96.86% Conservative: 1
Best Local Similarity: 96.54% Mismatches: 8
Query Match: 60, 04% Indels: 4
DB: 14 Gaps: 0

US-09-762-258-2 (1-495) x BQ059474 (1-1037)

QY 180 LeuGluAspThrAlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHis 199
Db 3 CTGGAAGATACGGCGCTGCTCTTACTGCTGAGATGACGCTGGCGCCCTGGCCATCTCCAC 62
QY 200 SerGlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGly 219
Db 63 TCCAGGGCATCATCTACACGGGACCTTCACCGGAAACATCATGCTCACACACCGGCG 122
QY 220 HisIleLysLeuThrAspPheGlyLeuCysLysGluSerIleHisGluGlyAlaValThr 239
Db 123 CACATCAAACTGACCCGACTTTCGACTGCAAGAGCTTTCATGAGGCGCCGCTACT 182
QY 240 HisThrPheCysGlyThrIleGluTyrMetAlaProGluIleLeuValArgSerGlyHis 259
Db 183 CACACCTTGTGGCGCACCATTTGATGATGCGCCCTGAGATCTGGTGGCCAGTGGCCAC 242
QY 260 AsnArgAlaValAspTyrTrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySer 279
Db 243 AACCGGCGCTGTGACTGTGTGAGCTGGGCGCCCTGTGTACACACATGCTCATGTGTCG 302
QY 280 ProPhePheThrAlaGluAsnArgLysLysThrMetAspLysIleIleArgLysLeu 299
Db 303 CCGCGCTTCCACCCGACAGAACCGGAAGAAACATGATGATCATCAGGCGCAAGCTG 362
QY 300 AlaLeuProProTyrLeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArg 319
Db 363 GCACGTGGCCCTTACCTCACCCAGATGCGCGGACCTTGTCAAAAAGTTTGTGAACGG 422
QY 320 AsnProSerGlnArgIleGlyGlyIleProGlyAspAlaAlaAspValGlnArgHisPro 339
Db 423 AATCCAGCCAGCGGATGGGTGGCCCGGAGGATGCTCTCATGTGACAGACATCC 482
QY 340 PhePheArgHisMetAsnTrpAspAspLeuAlaTyrArgValAspPropPheArg 359
Db 483 TTTTTCGGGACATGAAATTTGGAGACACTTCTGGCTGGGTGTGACCCCTTTACAG 542
QY 360 ProCysLeuGlnSerGluGluAspValSerGlnPheAspThrArgPheThrArgGlnThr 379
Db 543 CCTGTCTGAGTACAGAGGAGGAGTGTGAGCTTGTGATGATCCGCTTCACACGCGAGACG 602

OY	380	ProVlaaPserProAspAspThAlaLeuSerGIuSerAlaAsnGlnAlaPheIuGly	399
Db	603	CCGGGAGACAGTCCGATGACACACCCTCACGAGAGTGGCCAAACAGGCCCTTCTGGG	662
OY	400	PheTrTrYValAlaProSerValLeuAspSerIleYsgIuGlyPheSerPheGlnPro	419
Db	663	TTTCACATACGTGGCCCGCTCTGTCTTGACACAGATCAAGAGAGGCTTCTCTTCAGGCC	722
OY	420	LysLeuArgSerProArgArgLeuAsnSerSerProArgValProValSerProLeuLys	439
Db	723	AAGCGCCCTCACCCAGCGCCTCAACAGTACCCCCCGGGCCCCCGTACGCCCTCAAG	782
OY	440	PheSerProPheGluGlyPheArgProSerProSerLeuProGluProThGluLeuPro	459
Db	783	TTCTCCCTTTTGAAGGGGTTCGGCCACGCCCAACCTGGCGAGCCACGAGCTTACT	842
OY	460	LeuProProLeuLeuProProProProSerThrThrAlaProLeuProIleArgPro	479
Db	843	CTACCTCA-CTCCTGCGCAG-GGCGCGTCTCTGACAAAGGCCCTTCTCCATCGGTCC	900
OY	480	ProSer-GlyThrLysLysSerLysArg-GlyArgGlyArgProGluArg	495
Db	901	CCCTCAGGAGACCAAGAGTCCAAAAGGGGCGGCGGTTCAGGCGCG	950
RESULT 5			
LOCUS	BO052654	1014 bp	linear
DEFINITION	AGENCOURT_6871884 NIH_MGC_106 Homo sapiens	cdna	IMAGE:5934028
ACCESSION	BO052654		
VERSION	BO052654.1	GI:19811994	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	NIH-MGC http://mgc.ncl.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: c9apbs-remail.nih.gov		
	Tissue Procurement: Dr. Daniel McVicar, DBS/NCI		
	CDNA Library Preparation: Rubin Laboratory		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/ILNL at:		
	http://limage.llnl.gov		
	Plate: L16CM2119 row: 1 column: 05		
	High quality sequence stop: 703.		
FEATURES	Location/Qualifiers		
source	1..1014		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:5934028"		
	/clone_lib="NIH_MGC_106"		
	/tissue_type="natural killer cells, cell line"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: blood; Vector: pOTR1; Site_1: XhoI; Site_2:		
	EcoRI; cDNA made by oligo-dT priming. Directionally cloned		
	into EcoRI/XhoI sites using the following 5' adaptor:		
	GGCACGAG(G). Library constructed by Ling Hong in the		
	Laboratory of Gerald M. Rubin (University of California,		
	Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and		
	Superscript II RT (Life Technologies). Note: this is a		
	NIH_MGC library."		
BASE COUNT	225 a 312 c 278 g 197 t 2 others		
ORIGIN			
Alignment Scores:	3.92e-117	length:	1014
Pred. No.:			

Score:	1543.50	Matches:	312
Percent Similarity:	86.03%	Conservative:	2
Best Local Similarity:	85.48%	Mismatches:	18
Query Match:	59.05%	Indels:	33
DB:	14	Gaps:	2

US-09-762-258-2 (1-495) x B0052654 (1-1014)

QY	94	valPheGlnValArgLysValAlGInGlyThrAsn-LeuGlyLysIleTryAlaMetLysVal	113
DB	1	GGTTCCAGGTCGCGAAAGGTGCAGAGCACCAACTTNGCGCAAAATATATGCATTGAAGT	60
QY	113	lLeuArgLysAlaLysIleValAlaArgAsnAlaLysAspThrAlaHisThrArgAlaGlu	133
DB	61	CCTAAGGAAGGCCAAAAATTTGGCCCAATGCCMAAGACACAGCACAGGGCTGAGCC	120
QY	133	gAsnIleLeuGlnSerValLysHisProPheIleValGluIleuAlaTryAlaPheGlnTh	153
DB	121	GACACTTTTAAGTACAGTACGAAAGCACCCCTTATTGTGGAACTGGCCCTATGCTTCCAGAC	180
QY	153	rgLyLysLysLeuTryIleuIleLeuGlnLysLeuSerGlyGlyIleuLeuPheThrHisIle	173
DB	181	TGGTGGCAACGCTACCTCATCTTTGAGTGGCTCAGTGGTGGGAGCTTTCACGCATCT	240
QY	173	uGluArgGluGlyIlePheLeuGlnAspThrAlaCysPheTryIleuAlaGluIleThrIle	193
DB	241	GGAGCGAAGGGCATCTTCTCGGAAGATACGGCTGCTTACCTGGCTAGATCACGCT	300
QY	193	uAlaLeuGlnHisLeuHisSerGlnGlyIleIleCtyArgAspLeuLysProGluAsnI	213
DB	301	GGCCCTGGGCCATCTCCACTCCACAGGGCATATATACCGGGACCTCAAGCCCGAGAACAT	360
QY	213	eMetLeuSerSerGlnGlnHisIleLysLeuThrAspPheGlyLeuCysLysGluSerI	233
DB	361	CATGCTCAGACAGCGGCGCCACATCAACATGACCGACTTGGACTGTCGAAGAGCTCAT	420
QY	233	eHisGluGlyAlaValThrHisThrPheCysGlyThrIleGluTryMetAlaProGluI	253
DB	421	CCATAGAGGCGCCGCGCATCTCACACTTCTGGGGACCATTAGATACATGGCCCCCTGAT	480
QY	253	eLeuValArgSerGlyHisAsnArgAlaValAspTryTrpSerLeuGlyAlaLeuMetTy	273
DB	481	TCTGGTGGCGAGTGGCCCAACCGGGCTGTGGACTGGTGGACCTGGGGGCCCTTGATGT	540
QY	273	rAspMetLeuThrGlySerProProPheThrAlaGluAsnArgLysLysThrMetAspLy	293
DB	541	CGACATGCTCACTGGATGGCGGCCCTTCACCGCGAGACCGGAGAAACCATATGATTA	600
QY	293	sIleIleArgGlyLysLeuAlaLeuProProTyTryLeuThrProAspAlaArgAspLeuVal	313
DB	601	GATCTATCAGGGCGAAGCTGGCACTGCCCTTACCTCACCCACAGATGCCGGGACCTTGT	660
QY	313	lLysLysPheLeuLysArgAsnProSerGlnArgIleGlyGlyProGlyAspAlaAl	333
DB	661	CAAAAAGTTTCTGAAAACGAATCCACGCCACGGATTTGGGGGTGGCCAGGAGATGCTGC	720
QY	333	aAspValGlnArgHisProPhePheArgHisMetAsnTryAspAspLeuLeuAlaTrp	353
DB	721	TGATGTGCAGAAACATCCCTTTTCCGGCACATGAATTTGGAGACACTTCTGGCGTCGGC	780
QY	353	gValAspProPheArgProCysLeuGlnSerGluGlnAspValSerGlnPheAspTh	373
DB	781	TGTGAGACCCCTTTACAGGCCCTGTCTGCAGTGCAGAGSAGAGACGTGACCAATTGTGATAC	840
QY	373	rArgPheThrArgGlnThrProVal-AspSerProAspAspThrAla-LeuSerGluSer	392
DB	841	CCGCTTTCACAGGCGAGAACCCGGTGGGACATCTCTGATGCACAGCCCTTCAACAGAGT	900
QY	393	Ala-AsnGlnAlaPheLeuGlyPheThrTyValAlaProSerValLeuAspSerIleTy	412
DB	901	GCCCAACCAAGCCCTT-----	916
QY	412	sGluIlyPheSerPheGlnProLysLeuArgSerProArgArgLeuAsnSerSerProAr	432

[illegible][illegible]

|||||
Db 388 AAGGACACAGCAGACACAGGGGCTGAGCGAATCTTCTAGATGAGTGAAGCACCCTTT 447
OY 144 TLevalGluleuAlaTyraLapheGlnThrglyGlyLeuTyrlleuLleuGluCys 163
Db 448 ATTTGGAACTGGCCCTATCCCTCCAGACTGGTGGAACTCTACTCTCTTGGAGTGC 507
OY 164 LeuSerGlyGlyGlyLeuPheThrHisLeuGluArgGlyGlyIlePheLeuGluAspThr 183
Db 508 CTCACATGGTGGGAGACTCTTACACGATCTGAGACGAGGAGCATCTTCTGGAAAGTACG 567
OY 184 AlaCysPheTyrlleuAlaGluIleThrlleuAlaLeuGlyHisLeuHisSerGlnGlyIle 203
Db 568 GCCTCTTCTACTGGCTGAGATCAAGCTGGCCCTGGCCATCTCCATCCAGGAGCATC 627
OY 204 IleTyraArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeu 223
Db 628 ATCTACCCGGGACCTCAAGCCCGAAGACATCATCTCAGACGCGCAGCCACATCAAACTG 687
OY 224 ThrAspPheGlyLeuCysLysGluSerIleHisGlyAlaValThrHisThrPheCys 243
Db 688 ACCGACTTTGAGACTCTGCAAGAGTCTATCCATGAGGGGCGCTCATCACCCTTCTGC 747
OY 244 GlyThrIleGlyTyrcMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaVal 263
Db 748 GGCACCATTTGAGTACATGAGCCCTGATGATCTGATGATGATGATGATGATGATGATGAT 807
OY 264 AspTrpTrpSerLeuGlyAlaLeuMetTyraAspMetLeuThrglySer-ProProPheThr 283
Db 808 GACTGGTGGAGCCCTGGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 867
OY 283 rAlaGluAsnArg--LysLysThrMetAspLysIle-IleArgGly-----LysLe 299
Db 868 CGCAAGAAACCGGGAAGAAACCCCTGGGATAGATCCATCAGGCGGCAAGCTGGGAAGT 927
OY 299 uAlaLeuProProTyrlleuThrPro 307
Db 928 GGCC---CCCCCTAACNTCAACCC 949
RESULN 11
B0052262
LOCUS B0052262 1048 bp mRNA linear EST 29-MAR-2002
DEFINITION AGENCOURT_6868346 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5933480
5', mRNA sequence.
ACCESSION B0052262
VERSION B0052262.1 GI:19811602
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1048)
NIH-MGC htcp://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/MCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Place: LDCM2118 row: b column: 09
High quality sequence stop: 652.
Location/Qualifiers
1. 1048
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5933480"
/clone_lib="NIH_MGC_106"
/tissue_type="natural killer cells, cell line"

/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pORF7; Site: 1: XhoI; Site: 2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcorI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH-MGC Library."
BASE COUNT 259 a 303 c 290 g 195 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 1,21e-111 Length: 1048
Score: 1477.00 Matches: 299
Percent Similarity: 88.328 Conservative: 11
Best Local Similarity: 85.198 Mismatches: 27
Query Match: 56.508 Indels: 14
DB: 14 Gaps: 4
US-09-762-258-2 (1-495) x B0052262 (1-1048)
OY 53 GluProValGlyHisTyrlleuGluValGluLeuThrglyThrSerValAsnValGlyPro 72
Db 2 GAGCTGTGGGACACATATGAGAGGTGAGTACTGAGACGAGTGAACGCTTGGCCCA 61
OY 73 GluArgIleGlyProHisCysPheGluLeuArgValLeuGlyGlyGlyTyrlleu 92
Db 62 GAGCGCATGGGCGCCACGCTTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 121
OY 93 LysValPheGluValArgLysValGlnGlyThrAsnLeuGlyLysIleTyraMetLys 112
Db 122 AAGGTCTTCAGGTGGCAAGGTGCAAGGCACCACTTGGCAAAATATATGCAATGAA 181
OY 113 ValLeuArgLysAlaLysIleValArgAsnAlaLysAspThrAlaHisThrArgAlaGlu 132
Db 182 GTCTTAAGGAAGGCCCAAAATGTGCCAATGCCAAAGACACACACACAGCGCTGAG 241
OY 133 ArgAsnIleLeuGluSerValLysHisProPheIleValGluLeuAlaTyraLapheGln 152
Db 242 CGGAACATTTCTGAGTACATGAGCAACCCCTTATGTGGAACCTGCTTATGCTTCCAG 301
OY 153 ThrGlyGlyLysLeuTyrlleuLleuGluCysLysSerGlyGlyLysLeuPheThrHis 172
Db 302 ACTGGTGGCAAACTACTACTCATCTTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
OY 173 LeuGluArgGlyGlyIlePheLeuGluAspThrAlaCysPheTyrlleuAlaGluIleThr 192
Db 362 CTGGAGCGAGAGGGCATCTTCTCGAAGATAGCGGCTGCTTACTGCTGATGATCAG 421
OY 193 LeuAlaLeuGlyHisLeuHisSerGlnGlyIleIleTyraArgAspLeuLysProGluAsn 212
Db 422 CTGGCCCTGGGCAATCTTCACTCCAGGCAATCATCTTACCGGACCTCAAGCCCGGAAC 481
OY 213 IleMetLeuSerSerGlnGlyHisIleLysLeuThrAspPheGlyLeuGlyLysGluSer 232
Db 482 ATCATCTCTAGCAGCGAGGCGCCACATCAAACTGACCTTTGACTCTGCAAGAGTCT 541
OY 233 IleHisGlyGlyAlaValThrHisThrPheCysGlyThrIleGlyTyrcMetAlaProGlu 252
Db 542 ATTCATGAGGGGCGCTCACTACACCTTCTGGGCAACATTTAGATGAGGCGCTGAG 601
OY 253 IleLeuValArgSerGlyHisAsnArgAlaValAspTrpTrpSerLeuGlyAlaLeuMet 272
Db 602 ATTTGTGGTGGCAGTGGCCACAACCGGCTGTGATGATGATGATGATGATGATGATGATG 661
OY 273 TyraAspMetLeuThrglySerProProPheThrAlaGluAsnArgLysTyrlleuAsp 292
Db 662 TACGACATCTCACTAGTATGAGCGCCCTTACCGGCAAGAACCGGGAACCAATGAT 721
OY 293 LysIleIleArgGlyLysLeuAlaLeuProProTyrlleuThrProAspAlaArgsp--- 311
Db 722 AAGATCATCAGGGGCAAACTGGAGCTGCCCTTACTCACCACCAAAATGCGGGAACCT 781

QY 312 LeuValIysLysPheLeuLysArgAsnProSerGlnArg-ILeGlyGlyProGlyAs 331
 Db 782 TGTCAAAAAGTTTCTGAAACGAAATCCACCAAGCAATGGGGTGGCCAGGGGA 841
 QY 331 pAlaIleAspVal-GlnArgHisProPhePheArgHisMet-AsnTrpAspAspLeu 350
 Db 842 AGCTGCTGAAGTCCCAACATCCCTTTTCCGGCATGAATTTGGAAACAATTCTGT 901
 QY 351 -AlatPArg---ValAspProPheArgProCysLeu-----GlnSerGluGluAs 367
 Db 902 GGCTGTGGGGGGGGGACCCCTTTCAGGGCCTTGTCTTCACTCAAAAAGAAAGAAC 961
 QY 367 pValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSerProAspAspThr 387
 Db 962 TGGAAACCAATTGGA-----AACCCGCTTCCACCGCAAAAAG 1003
 QY 387 rAlaLeuSerGluSerAlaAsnGln 395
 Db 1004 CCGGGGGAAACAGTCCTCGAATGAA 1028

RESULT 12
 LOCUS AL527983 849 bp mRNA linear EST 13-FEB-2001
 DEFINITION AL527983 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC027YH21 5
 PRIME, mRNA sequence.
 ACCESSION AL527983
 VERSION AL527983.1 GI:12791476
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 849)
 TITLE Li,W.B., Gruber,C., Jessee,J., and Polayes,D.
 JOURNAL Full-length cDNA libraries and normalization
 COMMENT Unpublished (2001)
 CONTACT Genoscope
 GENOSCOPE Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 EMAIL: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES
 source
 1..849
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DC027YH21"
 /clone_1lb="LTI_NFL003_NBC3"
 /sex="male"
 /tissue_type="neuroblastoma cells"
 /lab_host="DH10B"
 /note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 178 a 242 c 268 g 159 t 2 others
 ORIGIN

Alignment Scores:
 Pred. No.: 7.46e-110 Length: 849
 Score: 1454.00 Matches: 279
 Percent Similarity: 99.29% Conservative: 0
 Best Local Similarity: 99.29% Mismatches: 2
 Query Match: 55.62% Indels: 0
 DB: 9 Gaps: 0

US-09-762-258-2 (1-495) x AL527983 (1-849)

QY 4 GlyArgArgAlaArgGlyAlaGlyAlaIleMetAlaIleValPheAspLeuAspLeuGlu 23
 Db 5 GGCCGACGGGGCCCGGGGGGGGGCCCATGCGGGCCCTGTTGATTTGGATTTGGAG 64
 QY 24 ThrGlnGluGlySerGlnGluGlnGluGluProGluLeuSerProAlaAspAlaCysPro 43
 Db 65 ACCGAGGAAGGACGACGGGCGAGGGCGACGACAGCTCAGCCCGCGGACGCAATGCC 124
 QY 44 LeuAlaGluLeuArgAlaAlaGlyLeuGluProValGlnHisTyrGlnGluValGluLeu 63
 Db 125 CTGGCCAGATTGAAGGAGAGCTGGGCTGAGACCTGTGGAGACATATGAAGAGTGGAGACTG 184
 QY 64 ThrGlnThrSerValAsnValGlyProGluArgGlyLeuProHisCysPheGluLeu 83
 Db 185 ACTGAGACCAAGCGGGAACGTTGGCCGAGAGCGCATCGGGCCCACTGCTTGGAGCTGCTG 244
 QY 84 ArgValLeuGluGlyLysGlyGlyTyrGlyValPheGlnValArgLysValGlnGlyThr 103
 Db 245 CGTGTGCTGGGCAAGGGGGGCTATGGCAAGGTGTTCCAGGTGCGAAGGTGCAGAGCACC 304
 QY 104 AsnLeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAla 123
 Db 305 AACTGGGCAAAATATATGCGCATGAAGTCCCTAAGAAAGCCAAATTTGGCCAAATGCC 364
 QY 124 LysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPhe 143
 Db 365 AAGGACACACACACACACGCGGTGAGCGGGAACATTTCTAAGTCAGTGAAGCACCCCTTT 424
 QY 144 IleValGluLeuValAlaTyrAlaPheGlnThrGlyGlyLysLeuTyrLeuIleLeuGluCys 163
 Db 425 ATTGTGGAACTGGCTTATGCTTTCAGACTGCTGGGCAAACTTCACTCATCTTGGAGTGC 484
 QY 164 LeuSerGlyGlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThr 183
 Db 485 CTCAGGTGTGGCGAGCTCTTCACGACATCTGAGAGAGAGGAGGACTCTCTGGAAGATAGC 544
 QY 184 AlacysPheTyrIleuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIle 203
 Db 545 GCCGTCTTCACTCGGTGGATGATCACGCTGGCCCTGGCCATCTCCACTCCAGGGGATC 604
 QY 204 IleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeu 223
 Db 605 ATCTACCGGGGACCTCAAGCCCGAGAACATATGCTGACGACCGGCGCATCAAACTG 664
 QY 224 ThrAspPheGlyLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCys 243
 Db 665 ACCGACTTTGGACTCTCAAGAGATCTATCCATGAGAGGGGCCCGTCACTCACACCTTCTGC 724
 QY 244 GlyThrIleGlyTyrMetAlaIleProGluIleLeuValArgSerGlyHisAsnArgAlaVal 263
 Db 725 GGCAACCAATTAGTACATGAGCCCTGAGATTCTGTGGTGGCCAGCCAGCGGGCTGTG 784
 QY 264 AspTrpTrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProPheThr 283
 Db 785 GACGGTGGAGCGCTGGGGCGCTGATGTATGACATGCTCAGCTGATGCGCGCCCTTACC 844
 QY 284 Ala 284
 Db 845 GCA 847

RESULT 13
 LOCUS B0890823 923 bp mRNA linear EST 16-AUG-2002
 DEFINITION AGENCOURT_8753030 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6394296
 5', mRNA sequence.
 ACCESSION B0890823
 VERSION B0890823.1 GI:22282837
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 923)


```
OY      4 GlyArgArgAlaArgGlyAlaGlyAlaAlaMetAlaAlaValPheAspLeuAspLeuGlu 23
      10 GGGCCAGCGGGCCGGGGGGCCGGCCCGCATGGGGCCGCTTTGATTGGATTGGAG 69
OY      24 ThrGluGluGlySerGluGlyGluGluGluProGluLeuSerProAlaAspAlaCysPro 43
      70 ACGGAGGAAGGCGACGAGGGCGAGGGCGAGCTCAGCCCGCGGACCATGTCC 129
OY      44 LeuAlaGluLeuArgAlaAlaGlyLeuGluProValGlyHisIleTyrGluGluValGluLeu 63
      130 CTGGCGAGTTGAGGGCGAGCTGGCTAGAGCTGTGGGACACTATGAAGAGGTGAGCTG 189
OY      64 ThrGluThrSerValAsnValGlyProGluArgIleGlyProHisCysSpheGluLeuLeu 83
      190 ACTGAGACCAAGGTGACGCTGGCCAGAGCCCATCGGGCCCATGCTTGTAGCTGCTG 249
OY      84 ArgValLeuGlyLysGlyGlyTyrGlyLysValPheGluValArgLysValGluGlyThr 103
      250 CGTGTGTGGGCGAGGGGGCTATGGCAAGGTTCAGAGTGCAGAAAGGTCCAGGACACC 309
OY      104 AsnLeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAla 123
      310 AACTTGGCCAAATATATGCTATGCAAGTCTTAAGGAAGCCAAATGTGCGCAATGCC 369
OY      124 LysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPhe 143
      370 AAGGACACAGCACACACACGGGCTGAGCGGAACATTCTAGAGTCACTGAGACACCCCTTT 429
OY      144 IleValGluLeuAlaTyrAlaPheGluThrGlyGlyLysLeuTyrLeuIleLeuGluCys 163
      430 ATTGTGGAACGTGGCTATGCTTCCAGACTGGTGCAAACTTACCTCATCTTGAGTGC 489
OY      164 LeuSerGlyGlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThr 183
      490 CTCAGTGTGGGAGCTCTTCACGATCTGGAGCGAGGCGCATCTTCCTGGAAAGATAGC 549
OY      184 AlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGluGlyIle 203
      550 GCGTCTCTTACCTGCTGAGATCACGCTGGCCCTGNGCCATCTCCACTCCACGGGCATC 609
OY      204 IleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGluGlyHisIleLysLeu 223
      610 ATCTACCGGAGCTCAGCCGAGAACATCATGCTCAGACGCGGCGCACATCAAACTG 669
OY      224 ThrAspPheGlyLeuGlySerIleHisGluGlyAlaValThrHisThrPheCys 243
      670 ACCGACTTGGACTCTGNCAGAGCTATCCATGAGGGGCGCTCCTCACACTTCTGTC 729
OY      244 GlyThrIleGluTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArg-AlaVal 263
      730 GGCACCATGTGAGTACATGAGCCCTAGATTCTGGTGCCGAGTGGCACACACGGGGCTGT 789
OY      263 AspTyrTrp-SerLeuGlyAlaLeu-MetTyrAspMet-LeuThrGlySer--ProPr 281
      790 GGACTGAGTGAAGCTGGGGGCGCTGAATGTACGACCTGGCTCACTGGGAATCGCCGCC 849
OY      281 PheThrAlaGlu-AsnArgLysLysThr-MetAspLysIleIleArgGlyLysLeu--- 299
      850 TTTCCCGCAGAAAAACCGAAAAAACCTTGATAGATCCTCAGGGGCAAACTGGGA 909
OY      300 AlaLeuProTyrLeuThrProAsp-AlaArg-AspLeuValLysLysPheLeuLys- 318
      910 ACTGCCCCCTTAACCTCAACCCCAATATGCCCCGGGACCTTGTCTCAAAAGTTTCCGANA 969
OY      319 --ArgAsnProSerGluArg--IleGlyGlyGly--ProGlyAspAla 332
      970 ACCGGAATTCACCCCGGGAATTGGGGGGGGGGCCCCCGGGAATGCC 1019
Db
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 18, 2002, 00:32:52 ; Search time 263 Seconds
(without alignments) 4238.552 Million cell updates/sec

Title: US-09-762-258-2
Perfect score: 2614
Sequence: 1 MARGRRAGCAAAVAEFDL.....PIRPPSGTKKSGRGRGRGR 495

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 segs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV-xlh
-O=/cgn2.1/USP70.spool/US09762258/runat_13112002_102444_4900/app_query.fasta_1.647
-DB=N.Geneseq_101002 -QFMT=fastlap -SUFPI=ring -MINMATCH=0.1 -LOOPL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Dlosum62 -TRANS=human40.cdi
-LIST=45 -DOCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09762258_ECGN_1.1_0.6runat_13112002_102444_4900 -KCPU=6 -ICPU=3
-NO_XLUPX -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONCLG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N.Geneseq_101002:*

- 1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
- 9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
- 17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
- 18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2614	100.0	1816	21 AAZ50703	p70(beta) S6 Kinas
2	2594	99.2	1732	24 AAD37031	Human p54S6K Kinas
3	2371	90.7	1647	21 AAZ87838	Human serine/threo
4	1947.5	74.5	1637	20 AAX61282	Human signal pepti
5	1748	66.9	2346	24 ABL65827	Lung cancer relate
6	1646	63.0	1197	21 AAF21858	Human breast and o
7	1455	55.7	2556	19 AAF19873	Drosophila p70S6K
8	1447.5	53.4	1898	23 ABL16561	Drosophila melanog
9	1385.5	53.0	1607	21 AAZ87837	Human serine/threo
10	1385.5	53.0	1609	21 AAZ35657	Human serine/threo
11	1383	52.9	6923	22 AAK86892	Human Immune/haema
12	1340	51.3	4357	22 AAK86891	Human Immune/haema
13	1211.5	46.3	843	22 AAH77989	Partial nucleotide
14	1149	44.0	12396	23 ABL16560	Drosophila melanog
15	966	37.0	3061	24 ABK83808	Human cDNA differe
16	966	37.0	3061	24 ABN95648	Gene #2146 used to
17	961	36.8	2791	20 AAZ09173	Human rsk3 cDNA.
18	961	35.8	2791	20 AAX84493	p90 ribosomal S6 k
19	958	36.6	5673	24 AAS94865	Human DNA sequence
20	949.5	36.3	2260	17 AAT27730	Insulin-stimulated
21	949.5	36.3	2260	24 ABK84208	Human cDNA differe
22	948.5	36.3	2260	17 AAT27731	Human cDNA differe
23	937.5	35.9	2238	22 AAF44637	Mutant Insulin-sti
24	934	35.7	3203	23 ABL25555	Novel protein Kina
25	934	35.7	5656	23 ABL25554	Drosophila melanog
26	907.5	34.7	3120	21 AAI10529	Mitogen and stress
27	907.5	34.7	3225	21 AAZ46159	cDNA sequence enco
28	896.5	34.3	3400	22 AAK51952	Human polynucleoti
29	886.5	33.9	3131	21 AAI10533	Mitogen and stress
30	878.5	33.6	2134	21 AAI10542	Mitogen and stress
31	873.5	33.4	2116	21 AAI10543	Mitogen and stress
32	873.5	33.4	2117	21 AAI10530	Mitogen and stress
33	872.5	33.4	2134	21 AAI10531	Mitogen and stress
34	866.5	33.1	3132	22 AAK52936	Human polynucleoti
35	847	32.4	3165	23 AAS84870	DNA encoding novel
36	844	32.3	594	23 AAS19264	Human cDNA encodin
37	841.5	32.2	1230	23 AAS84869	DNA encoding novel
38	840	32.1	2222	21 AAI10532	Mitogen and stress
39	813.5	31.1	673	21 AAF15983	Human prostate can
40	810.5	31.0	2281	20 AAZ33647	Human breast tumou
41	806.5	30.9	1296	22 AAF44639	Novel protein Kina
42	806.5	30.9	2346	20 AAV74190	Human sgk DNA. Ho
43	806.5	30.9	2370	19 AAV48311	Human cell-volume
44	806.5	30.9	2370	24 ABK84749	Human cDNA differe
45	806.5	30.9	2370	24 ABN97360	Gene #3858 used to

ALIGNMENTS

RESULT 1
AAZ50703
ID AAZ50703 standard: DNA: 1816 BP.

AAZ50703;
31-MAY-2000 (first entry)

p70(beta) S6 kinase gene.

p70 (beta) S6 kinase; p70betas6k; ribosomal protein kinase; S6 protein;
cellular signalling; probe; ribosomal activity; cellular proliferation;
cytostatic; ss.

OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 77..1564
FT

Db	1397	TCCTCTTTTGAAGGGTTTCGGCCCA6GCCACCTCCGGAGCCACGAGACTACTCTTA	1456
Oy	461	ProPoleuLeuProProProProProSerThrThraLaProLeuProIleArgProPro	480
Db	1457	CCTCAGCTCTGTCCACACGGCGCGCCGCTCGACACACGGCGCCCTCTCCATCGTCCGCC	1516
Oy	481	SerGlyThrLysLysSerLysArgGlyArgGlyArgProGlyArg	495
Db	1517	TCAGGGACCAAGAAAGTCCAGAGGGGCGGTGGCGTCCAGGGCGC	1561
RESULT 2			
ID	AAD37031		
AD37031	standard; DNA; 1732 BP.		
AC	AAD37031;		
XX			
DT	27-AUG-2002 (first entry)		
DE			
XX			
DE	Human p54S6K DNA.		
XX			
KW	Human; mammalian kinase: p54S6K; p85S6K; antibody generation; cancer;		
KM	diagnosis; drug identification; cytostatic; enzyme; gene; ds.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	36..1484	
FT		/*tag=	
FT		A	
FT		/product= "Human p54S6K protein"	
XX			
PN	US6372467-B1.		
XX			
PD	16-APR-2002.		
XX			
PF	29-OCT-1999;	99US-0430564.	
XX			
PR	29-OCT-1998;	98US-106414P.	
XX			
PA	(HARD) HARVARD COLLEGE.		
XX			
PI	Blenis J, Lee-fruman KK, Kuo CJ;		
XX			
DR	WPI: 2002-424732/45.		
XX	P-PSDB: AAE23306.		
XX			
PT	Isolated mammalian p54S6K and p85S6K kinases, useful for diagnosing and		
PS	treating cancers -		
XX			
XX	Example 1: Fig 1A; 30pp: English.		
XX			
CC	The invention relates to mammalian kinases, p54S6K and p85S6K and		
CC	methods for identifying compounds that modulate, or which are modulated		
CC	by p54S6K and p85S6K. The p54S6K and p85S6K kinases may be used as		
CC	antigens to generate antibodies that may be used in immunoassays to		
CC	detect and quantitate the presence of p54S6K and p85S6K kinases in		
CC	samples and therefore be used to diagnose diseases, e.g. cancers. They		
CC	may also be used in assays as drug targets to identify potential drugs		
CC	for the treatment of diseases associated with p54S6K and p85S6K kinase		
CC	expression and activity. The present sequence is human p54S6K DNA.		
XX			
XX			
SO	Sequence 1732 BP; 355 A; 532 C; 532 G; 313 T; 0 other;		
Alignment Scores:			
Pred. No.:	9.86e-167	Length:	1732
Score:	2594.00	Matches:	491
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.23%	Indels:	0
DB:	24	Gaps:	0

QY	5	ArghrghlaaarggylaglylaaglylaalamefialaialvalPheaspheuaaspheunthr	24
Db	9	CGAGGGGGCCCCGGGGGGGGCGCGCCATGGCGGGCGCTTTTGATTGGATTGGAGACG	68
QY	25	GlugluglysergyluglygluglygluProgluIdeuserProalAaspIacyProeu	44
Db	69	GAGGAGGCGACCGAGGGCGAGGGCGAGCCAGACCTAGCCCCCGGAGCGCATGTCCCTT	128
QY	45	AlaGlueuArGaLaalaglyleugluProvalGlyhIstfclugluValGlueuthr	64
Db	129	GCCGAGTTGAGAGGCAAGCTGGCTTAGAGACCTGTGGACACTAGAAAGAGGTGGAGCTGACT	188
QY	65	GluthrserValasnValGlyProgluArgTleGlyProhiscysPheglueuArg	84
Db	189	GAGACACGCGGAACGTGGGCCAGAGCCGATGGGGCCCCACTGCTTTAGCTGTGGCT	248
QY	85	ValleuglyLysgLygLygLygLygValPhegluValArgLysValGlnGlyThrAsn	104
Db	249	GTGCTGGGCGAAGGGGGGCTTAGCCAGAGTTCCTCAGGTGCGAAGGTGCAGGCCAAC	308
QY	105	LeuglyLysIleYrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLys	124
Db	309	TTGGGCAAAATATATGCGCATGAAAGTCCTAAGAGAGCCAAATGTGGCAATGCCAAG	368
QY	125	AsphrAlaHisThrArgAlaGluArgAsnIleleugLuserValLysHisProphelle	144
Db	369	GACACAGCACACACCGCGGTGAGCGGACATCTAGACATGTAGAGACACCCCTTTATT	428
QY	145	ValGluuAlaYrAlaIapheglInthGlyLysLeuYrLeuIleleuGluYrLeu	164
Db	429	GTGGAACTGGCTATGTGCTTCACAGCTGGGGGAAACTTACTTCACTCTTAGTGCTC	488
QY	165	SergLygluLeuapheThrHisLeuGluArgGlyIlePheleugluAspPhrAla	184
Db	489	AGTGTTGGCGAGCTCTTCACAGCATCTGAGACGAGAGGCACTCTCTGGAATATAGGCC	548
QY	185	CysPheYrLeuAlaGluIlethrLeuAlaLeuGlyHisLeuHisSergInglyIlele	204
Db	549	TGCTTCTACCTGCGTGAATCAGCGTGCGCCCTGGCGCATCTCCACTCCAGCGGCATATC	608
QY	205	TyrTrgAspLeuLysProgluAsnIleMetLeuSergInglyHisIleLysleuthr	224
Db	609	TACCGGAGCTCAAGCCCGGAACATATCTAGCAGCGCAGGCGCACATCAACTGAC	668
QY	225	AspPhegluLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysgly	244
Db	669	GACTTGGACCTCGACAGAGTCTATCCATGAGAGGGCGCGTCACTACACCTTCGCGCG	728
QY	245	ThrIleGlyrMetAlaProgluIleLeuValArgSergIlyHisAsnArgAlaValasp	264
Db	729	ACCATTTGATGATCAGGCCCTGTGATTTCTGTGCGAGTGGCCACACCGGGCTGTGAC	788
QY	265	TrpTrpSerLeuGlyAlaLeuMetYrAspMetLeuThGlySerProprophethrAla	284
Db	789	TGTGTGACCTCGGGGGCGCTGATGTATGACATCTCTACTGATCGCGGCTTTACCGCA	848
QY	285	GluAsnArgLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProProYr	304
Db	849	GAGAACCGGAAGAAACCATGATGATATCAGGGCGACAGCTGGCATGTGCCCTTAC	908
QY	305	LeuthrProaspAlaArgaspLeuValLysLysPheLeuLysArgAsnProSergInaYr	324
Db	909	CTCACCCAGATGCGCGGAGCACTGTCAAAAATTCTTGTAAGCGAATCCAGCCAGCGG	968
QY	325	IleGlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisProphethrArgHisMet	344
Db	969	ATTGGGGGTGGCCAGGGGATGCGTCGATGTCACAGACATCCCTTTTCCGGACATG	1028
QY	345	AsnTrpAspAspLeuAlaIATrPArgValAspProProPheArgProCysLeuGlnSer	364
Db	1029	AATTGGACACACTTTCGTGGCTGGCGGTGTGAGACCCCTTTCAGGCGCTGTGCAGTCA	1088
QY	365	GlugluAspValSergInPheAspThrArgPheThrArgGlnThrProValAspSerPro	384


```
QY 244 lythrlleglutyrmatalaprocluilileuvalarsergilyhisasnargalaval 264
|||
DB 648 GCACCATTTGAGTACATGGCCCCCAGANTCTGGTGGCGAGTGGCCACACGGGGGTGG 707
QY 264 sprtprpserleuglyalaleuemetlyrasmetleuthgilyserprobrophethra 284
|||
DB 708 ACTGGTGAGAGCTGGGGCCCTGATGTACAGACATGCTACATGATGATGCGCCCTTACCG 767
QY 284 laagiuaanarglylsythmetasplyslielleargglylylsleualaleuaprobror 304
|||
DB 768 CAGAGAACCGGAGAAACCATGTGATGATCATCAGGGGCAACCTGGCACTGGCCCCCT 827
QY 304 yrlleuthrproaspalaarqaspleuvallylslyspheleuylarqasndrosergina 324
|||
DB 828 ACCACACCCCGAGATGCCGGGACCTTGTCATAAAAGTTTCTTAACGGATCCAGCCAGC 887
QY 324 rglleglyglylyproglyaspaalalaaspaalalarghisprophetharghism 344
|||
DB 888 GGATTTGGGGGTGGCCAGGGGATGCTGCTGATGTGCAGAGACATCCCTTTTCCGGCACA 947
QY 344 etasntppaspspleuualatrpargvalaspproprophethargproclystleugins 364
|||
DB 948 TGAATTTGGAGAGACCTTCTGTGGCTGGGTGGACCCCTTTGAGGCCCTGTGTGCAGT 1007
QY 364 ergluciuaspvalserclynpheasprthrargphethrarglnthrprovalaspsr 384
|||
DB 1008 CAGAGGAGAGAGCTGAGCCAGTTTATACCCGCTTACACGGGCAAGCGGGGTGGACATTC 1067
QY 384 roaspasprthrAlaleuSERgluSERalaaSnglnAlaPheleuglyphethrTyrrValA 404
|||
DB 1068 CTGATGTACACAGCCCTCAGCAGAGAGTGCACACAGGCTTCTGTGGCTTCAATACGTGG 1127
QY 404 laProserValleuaspsrlielyslygluylpheserPhegluProlysleuaurSerP 424
|||
DB 1128 CGCGGTCTGTCTGTGACAGCATCAAGAGGGCTTCTCTTCCAGGCCCAAGTGGCGTTCAC 1187
QY 424 roATgArGLeuaSnSerSerProArGValProValSerProleuylsPheSerPropheg 444
|||
DB 1188 CCAGGGCGCTCAACAGTAGACCCCGGGGTCCCGTCAGCCCTCAAGTTCCCTTTTGG 1247
QY 444 luGllyPheahgProSerProSerleuProgluProthhGluLeuProleuProleuL 464
|||
DB 1248 AGGGGTTTCGGCCAGCCGCCAGCTGCGGAGGCCACGAGCTACCTTACCTCCACATCC 1307
QY 464 eupProProProProSerSerhthrAlaProleuProliIaargProbrosergilyhrl 484
|||
DB 1308 TGCCACCGCGCGCCCTCGACACACCGCCCTCTCCATCCGTCCTCCCTCAAGGACCA 1367
QY 484 yslYserlYsArGLYArGLYArGProGLYArG 495
|||
DB 1368 AGAGTCCAGAGAGGGGGCTGGGGCTCCAGGGCCG 1402
RESULT 4
AAK61282
ID AAK61282 standard; cDNA; 1637 BP.
XX
AC AAK61282;
XX
DT 29-JUL-1999 (first entry)
XX
DE Human signal peptide-containing protein encoding cDNA seq ID NO:10.
XX
KW Human; signal peptide-containing protein; SP; cell proliferation;
KW cancer; neuronal disorder; immune response; detection; ss.
XX
OS Homo sapiens.
XX
PN MO9924463-A2.
XX
PD 20-MAY-1999.
XX
PF 04-NOV-1998; 98WO-US23578.
XX
```

```
PR 07-NOV-1997; 97US-0966316.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Au-Young J, Lal P, Mathur P, Murry LE, Reddy R;
DR WPI; 1999-337694/28.
XX
PT cDNA clones encoding signal peptide-containing proteins
PS Claim 4; Page 75-76; 83pp; English.
XX
CC The present sequence represents a human cDNA clone encoding a signal
CC peptide-containing protein (SP). SP proteins can be used to stimulate
CC cell proliferation or to treat or prevent cancer. SP antagonists are
CC also used to treat or prevent cancer, and also for treating or
CC preventing neuronal disorders or immune responses. Polynucleotide
CC sequences complementary to the SP-encoding polynucleotides are useful
CC for the detection of SP-encoding nucleic acid molecules in biological
CC samples.
XX
SQ Sequence 1637 BP; 342 A; 473 C; 463 G; 332 T; 27 other;
Alignment Scores:
Pred. No.: 5.53e-123 Length: 1637
Score: 1947.50 Matches: 407
Percent Similarity: 90.89% Conservative: 2
Best Local Similarity: 90.44% Mismatches: 34
Query Match: 74.50% Indels: 13
DB: Caps: 4
US-09-762-258-2 (1-495) x AAK61282 (1-1637)
QY 9 GlyalaglyAlaAlaMetAlaAlaValPheaspLeuaspleuGluthrGluclySer 28
|||
DB 180 GGGGGCGGGCGCGCATGCGCGCCGCTGTTGGATTGGAGACGAGAGAGAGAGCAGC 239
QY 29 GluGllygluGllygluProgluLeuSerProAlaAspAlaCyProleuAlagluLeuArg 48
|||
DB 240 GAGGGCGAGGGGAGCCAGAGCTCAGCCCCCGGACGATGTCCCTTCCGAGTTGAGG 299
QY 49 AlaAlaglyLeuGluproValglYhlsTyrgluGlualValgluLeuthrGluthrSerVal 68
|||
DB 300 GCAGCTGGCCATGAGACCTGTGGGACATATGAAAGGAGTGGAGCTGATGAGACAGCGCG 359
QY 69 AsnValglYProgluArgIleglYProhiscYsPhegluLeuLeuArgValleuglylys 88
|||
DB 360 AACGTTGGCCAGAGCGCATGCGGGCCCACTGCTGTGAGCTGCTGCTGGGCAAG 419
QY 89 GlyglYTyrglylsYValPhegluValArglylsValInglyThrAsnleuglylsyle 108
|||
DB 420 GGGGGCTATGGCAGAGGTTCAGGTGGGAAAGTGCACAGCCACCACTTGGGCAAAATA 479
QY 109 TyralaMetlylsValleuArglylsAlaYlsIleValaArgasnalalysAspThrAlahls 128
|||
DB 480 TATGCCATGAAGAATCTTAAGAGAGGCCAAATTTGGCCGAATGCCAAGAGACACACACAC 539
QY 129 ThrArgAlaGluArgAsnIleleuGluservAllyshsProphleIleValgluLeuAla 148
|||
DB 540 ACACGGCGTGAAGCGGAMATCTTACAGTCAGAGACACACCCCTTATGTGTGMACTGGCC 599
QY 149 TyralaPheglInThrGlYlylsleuthrleuile-leuGlucYsleuSerGlyglYl 168
|||
DB 600 TATGCTTCCAGACTGAGTGGCAAACTTACCTTGAATTCCTTCAAGTGGGGGCA 659
QY 168 uleuphethrhlsleuGluarGluGlYlIlePheleuGlusprthrAlaCySPheTyrlle 188
|||
DB 660 GCTCTTCAAGCATCTGGAGCGAGAGGATCTTCTGTGAAGATAGGGCTGTTCTACT 719
QY 188 uAlagluIlethrleuAlaleuGlYhlsleuHlsSerInglylleIleTyrrArgAsple 208
|||
DB 720 GGCTGAGATCAAGCTGGGCGCATCTCCATCTCCACGCCAGGCAATCAATCCGGGACCT 779
```

QY 208 ulyspProgluAsnIleMetLeuSerSergInglyHisIleLeuThrAspPheGlyLe 228
 DB 780 GAGCCCGAGAACATCATCTCTCAGCAGCAGGCCACATCAACTGACGACTTGGACT 839
 QY 228 ucysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThrIleGly 248
 DB 840 CTGCAGAGAGTCTATCATGAGGGGCCCGCTCATCTCACCCTTGGGGCCATTGAGTA 899
 QY 248 rMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTrpPse 268
 DB 900 CATGGCCCTGAGATCTGTGGTGGCAGTGGCCCAACCGGGCTGTGAGCTGGAGCCT 939
 QY 268 uGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThrAlaGluAsnArg 288
 DB 960 GGGGGCCCTGATGTACGACATGCTCACTGGATGGCCGCTTACCGCAGAGAACCGGAA 1019
 QY 288 slysrThrMetAspLysIleIleArgGlyLysLeuAlaLeuProProTyrLeuThrPro 308
 DB 1020 GAAGACCATGAGTAATCATCATCAGGGGCAAGCTGGCAGCTGCCCTTACTCATCCACGA 1079
 QY 308 pAlaArgAspLeuValLysLysPheLeuLysArgAsnProSergIArgIleGlyLys 328
 DB 1080 TGGCCGGGACCTTGTCAAAAAGTTTCTGAACGAGATCCACGACGAGATTGGGGGTG 1139
 QY 328 yProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMetAsnTrpAsp 348
 DB 1140 CCCAGGGGATGCTGCTGATGTGCAGACATCCCTTTTCCGACATGAAATTGGAGCA 1199
 QY 348 pleuLeuAlaTrpArgValAspProPhe-ArgProCysLeuGlnSerGluGluAsp 368
 DB 1200 CTT-CTGGCCCTGGCTGTGGANCCCCCTTTCAGGCCCTGTGTGCAGTCAAGAGACG 1258
 QY 368 alSergIlePheAspThrArgPheThrArgGlnThrProValAspSerProAspPThr 388
 DB 1259 --GAGAGTTTGATACCCGCTTCACAGCGAGAGCGCGGTGACATCCGATGACACAG 1316
 QY 388 lalSerSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTyrValAlaProSerVal 408
 DB 1317 C-CTCAGCAGAGTGGCAACAGGCTCTGTGGGTT-ACATAGAGCGCGC-TCGTTC 1373
 QY 408 euAspSerIleLysGluGlyPheSerPheGlnProLysLeuAspSerProArgArgLeu 428
 DB 1374 TGGACAG-ATCAAGAGG---TTCTCTTTCAGCCCAAGT-----GGGTCAACCGAGGCTC 1423
 QY 428 snSerSerProArgValProValSerProLeuLysPheSerProPheGluGlyPheArg 448
 DB 1424 AANATAGCCCCGGG---TCCGTNAGCCCC---TCAAGTTTNNCCCTTNNAGGTTGGGCCA 1477
 QY 448 roSerProSerLeuProGluProThr 456
 DB 1478 GCCACCTTNCNGGCCAGAGTACT 1503
 RESULT 5
 ABL65827
 ID ABL65827 standard. DNA; 2346 BP.
 XX
 AC ABL65827;
 XX
 DT 15-MAY-2002 (first entry)
 XX
 DE Lung cancer related gene sequence SEQ ID NO:4164.
 XX
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200194629-A2.
 XX
 PD 13-DEC-2001.
 XX

PF 30-MAY-2001; 2001WO-US10838.
 XX
 PR 05-JUN-2000; 2000US-209473P.
 PR 05-JUN-2000; 2000US-209531P.
 PR 18-SEP-2000; 2000US-233133P.
 PR 18-SEP-2000; 2000US-233617P.
 PR 20-SEP-2000; 2000US-234009P.
 PR 20-SEP-2000; 2000US-234034P.
 PR 20-SEP-2000; 2000US-234052P.
 PR 22-SEP-2000; 2000US-234509P.
 PR 22-SEP-2000; 2000US-234567P.
 PR 25-SEP-2000; 2000US-234923P.
 PR 25-SEP-2000; 2000US-234924P.
 PR 25-SEP-2000; 2000US-235077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 25-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.
 (AVAL-) AVALON PHARM.
 PA Young PE, Augustus M, Carter KC, Edner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 DR
 XX
 DR
 XX
 PT
 PT
 PS
 PS
 XX
 Claim 1; SEQ ID 4164; 44pp; English.
 Screening for anti-neoplastic agent involves exposing cells to a
 chemical agent to be tested for anti-neoplastic activity, and
 determining a change in expression of a gene of a signature gene set -
 Claim 1; SEQ ID 4164; 44pp; English.
 The present invention describes a method (M1) for screening for an
 anti-neoplastic agent. The method involves exposing cells to a chemical
 agent to be tested for anti-neoplastic activity, determining a change in
 expression of at least one gene (I) of a signature gene set, where (I)
 comprises a sequence (S) selected from 8447 sequences (given in ABL6164
 to ABL7110), or is at least 95% identical to (S), where a change in
 expression is indicative of anti-neoplastic activity. (I) has cytostatic
 activity and can be used in gene therapy. M1 can be used for screening
 an anti-neoplastic agent, and can be used for producing a product which
 is the data collected with respect to the anti-neoplastic agent as a
 result of M1, and the data is sufficient to convey the chemical
 structure and/or properties of the agent. M1 can be used in the
 treatment of cancer such as colon, breast, stomach, lung, thyroid,
 oesophageal, ovarian, prostate or pancreatic cancer,
 adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,

CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.

carcinoma, papillary carcinoma and Wilms' tumour.

SQ Sequence 2346 BP; 750 A; 453 C; 558 G; 585 T; 0 other;

Alignment Scores:

Pred. No.:	2,67	109	length:	236
Score:	1748	00	Matches:	354
Percent Similarity:	73.45		Conservative:	50
Best Local Similarity:	64.35		Mismatches:	80
Query Match:	66.87		Indels:	66
DB:	24		Gaps:	8

US-09-762-258-2 (1-495) x ABL65827 (1-2346)

[illegible]

Db	856	TGGAGCTTGGAGACATTAAATGATATGACATGCTGACGTGGAGACACCCCAATCTACTGGGAG	915
QY	286	AsnArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProProTyrLeu	305
Db	916	AATGAAAGAAAGAAACAATTGGACAAAATCTCAATGTAACTCAATTGGCTCCCTACCTC	975
QY	306	ThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProPheGlnArgIle	325
Db	976	ACACAAAGACGACAAAGATGCTTAAATAAACCTGCTTAAAGAAATGCGCTTCGTCTG	1035
QY	326	GlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisIleProPhePheArgHisMetAsn	345
Db	1036	GGAGCTGCTCTGGGGAGCGCTGGAGAAAGTTCAAGCTCATCTATTCTTTAGACACTTAAAC	1095
QY	346	TrpAspAspLeuLeuAlaIleIleArgValAspProProPheArgProCysLeuGlnSerGlu	365
Db	1096	TGGGAAGAATCTTGTGGCTGCAGAAAGTGGAGACCCCTTAAACCTGTGTGCAATCTGAA	1155
QY	366	GluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSerProAsp	385
Db	1156	GAGGATGTAAATCGATTGTGATTCACAAATTACACGTCACACACCTGTGCAGCCCAAT	1215
QY	386	AspThrAlaLeuSerGlnSerIleLysGlnGlyPheSerPheGlnProLysLeuArgSerProArg	405
Db	1216	GACTCACTCTCATGTAGAAAGTGCACATCAGCTTTTCTGGGTTTACATATGTGCTCTCA	1275
QY	406	SerValLeuAspSerIleLysGlnGlyPheSerPheGlnProLysLeuArgSerProArg	425
Db	1276	TCTGTACTTGAATGTGTAAGAAAGATTTTCTTCTTGAACCAAAAATCGATCACCTCGA	1335
QY	426	ArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerPro-----Phe	443
Db	1336	AGATTATTATGGACACCCACGACAAACCTGTCAGCCAGTCAAAATTCTCTCGGGATTTC	1395
QY	444	GluGlyPheArgProSerProSerLeuProGluProThrGluLeuProLeuProLeu	463
Db	1336	TGGGAGACAGCTGCTTGGCCAGC-----ACAGCAATCTCAGACACCTGTG	1443
QY	464	LeuProProProProProSer-----Thr	471
Db	1444	GAATACCCCAATGGAACAAAGGCGCATGAGCACAATGGATGTGACATGATGGGGAACGA	1503
QY	472	ThrAlaProLeuProIleArgProProSerGlyThrLys-----	484
Db	1504	TGCGACACACTTCCAAATACACAGACCGCAACTGTGGCCATACAAAAACAACCTTTTCCC	1563
QY	484	-----	484
Db	1564	ATGATCTCCAAAGCGCAGACACCTGCGTATGATCTATGACAGACAAATCTTTTAAT	1623
QY	485	-----LysSerLysArgGlyArgGlyArg	492
Db	1624	GAATTTAAAGCAAAAAGGTGGAGAGGAGCA	1653
RESULT 6			
AAF21858			
ID	AAF21858 standard; DNA; 1197 BP.		
XX	AAF21858;		
XX	27-MAR-2001 (first entry)		
DE	Human breast and ovarian cancer associated antigen gene SEQ ID 245.		
XX	Human; breast cancer; ovarian cancer; cyrostatic; immunosuppressive;		
KM	nootropic; neuprotective; antiviral; antiallergic; hepatotropic;		
KM	antidiabetic; antiinflammatory; antitumor; antitumor; anticonvulsant;		
KM	antibacterial; antifungal; antiparasitic; cardiant; immune disorder;		
KM	Addison's disease; allergy; autoimmune hemolytic anaemia;		
KM	autoimmune thyroiditis; diabetes mellitus; Crohn's disease;		
KM	multiple sclerosis; rheumatoid arthritis; ulcerative colitis;		
KM	cardiovascular disorder; wound healing; neurological disease; ds.		
XX			

PA (NOVS) NOVARTIS AG.
XX Kozma S, Stewart M, Thomas G;
XX WPI: 1998-120783/11.
DR P-PSDB; AAM52294.
XX New Isolated Drosophila p70 S6 kinase - is used to develop products
PT for studying the kinase signalling pathway and for modulating the
PT kinase activity
XX
PS Claim 3; Page 38-42; 47pp; English.
XX
CC This sequence encodes the Drosophila p70 S6 Kinase (p70S6) of the
CC invention. The products are used in the study of the p70 S6 kinase
CC enzyme. They can be used for defining the p70 S6 kinase signalling
CC pathway and to develop agents for modulating the kinase activity. The
CC products can also be used for the production of antibodies and for
CC detection.
XX
S0 Sequence 2556 BP; 717 A; 663 C; 643 G; 533 T; 0 other;

Alignment Scores:
Pred. No.: 2.03e-89 Length: 2556
Score: 1455.00 Matches: 309
Percent Similarity: 66.73% Conservative: 52
Best local Similarity: 57.12% Mismatches: 115
Query Match: 55.66% Indels: 65
DB: 19 Gaps: 10

US-09-762-258-2 (1-495) x AAV19873 (1-2556)
QY 13 ALaMetAlaAlaVal-----PheaSplLeu-----AspLeuGlu 23
Db 471 GCATGGCGGAGCTGAGGATCCCGACGACTGTTGACCTGGAGCTGCACCGCTGGAA 530
QY 24 ThrGluGluGlySerGluGlyGluGluPro-----GluLeuSerProAlaAsp 40
Db 531 CTGCAGCAGCAAGGCCAGGACTCGCAGCAGCAGAGATGAGCTGGACGACGTTGAC 590
QY 41 AlaCysProLeuAlaGluLeuArgAlaAlaGlyLeuGluProValGlyHisTyrGluGlu 60
Db 591 CTAGAACC-----GAATTGTGTATTAATCTGCACCAAGCACTGAGGCCAGGACC 644
QY 61 ValGluLeuThrGluThrSerValAsnValGlyProGluArgIleGlyProHisCysPhe 80
Db 645 ATACGCTCTGCGAGGAGAAATGTTATCCAGGTAATAATCAAGTGGACCCAGACTTT 704
QY 81 GluLeuLeuArgValLeuGlyLysGlyLysGlyTyrGlyLysValPheGluValArgLysVal 100
Db 705 GAGCTCAAGAAAGTCTTGGCAAGCGGTTATGGCAAGTATTTCAGGTGGCCAAAGACC 764
QY 101 GlnGlyThrAsnLeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleVal 120
Db 765 GCTGGACACGAGTGTACAAATAATTTTCCATGAGAGTGCTCAAAAAGGCATCCATTGTG 824
QY 121 ArgAsnAlaLysAspThrAlaHisThrArgAlaGluIleuArgAsnIleLeuGluSerValLys 140
Db 825 ACCAATCAAAAGGACACGCGACACCGCGCGCGCAAGCGCAATATCTCGAGGCACTGAAG 884
QY 141 HisProPheIleValGluLeuAlaTyrAlaPheGlnThrGlyLysLysLeuTyrLeuIle 160
Db 885 CATCCCTTCATAGTGGACTAGTTATGCTTCCAGACAGACGAGAAACTATACCTTTAA 944
QY 161 LeuGlyCysLeuSerGlyGlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeu 180
Db 945 CTGGAATATCTCAGCGGTGGAGCTGTTCATGCACTTGGAGCGTGAGGGCATCTTCTTA 1004
QY 181 GluAspThrAlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSer 200
Db 1005 GAGGATACCACTGCTTCTATCTTAAGCGAAATCATTTTGGCTTGGCCATTACACAA 1064
QY 201 GlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHis 220

Db 1065 CTGGGCAATCATCTACCGGATCGAAGCCGGAACATCTCTCGATGCACAGGACAT 1124
QY 221 IleLysLeuThrAspPheGlyLeuCysLysGluSerIleHisGluGlyValAlaThrHis 240
Db 1125 GTGAAGCTCAGCGACTTGGACTGTGCAAGGAGCACATCAAGAGGTATTTGCACCCAC 1184
QY 241 ThrPheCysGlyThrIleGluTyrMetAlaProGluIleLeuValArgSerGlyHisAsn 260
Db 1185 ACCTTCTGCGGACAAATTCATGATGACCTGAAATTTTACCAAGATGGCCATGCC 1244
QY 261 ArgAlaValAspTyrTrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerPro 280
Db 1245 AAGACAGTCACTGTGTGTCACCTGGCGCTCATGTTGATGATGCTCAGAGTCCCA 1304
QY 281 ProPheThrAlaGluAsnArgLysTyrThrMetAspLysIleIleArgGlyLysLeuAla 300
Db 1305 CCCTTCACCGCGGAATTCGCAAGAACATCGAGACCATTCGTGAAGCCAGGTCAT 1364
QY 301 LeuProTyrLeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsn 320
Db 1365 CTGCCAGCTTACCTTACACCGGAGAGCGGATCTGTGTCTGCTGCTGTGAAGCGCAG 1424
QY 321 ProSerGlnArgIleGlyGlyLysProGlyAspAlaAlaAspValGlnArgHisProPhe 340
Db 1425 GAACCTCAGCGGCTTGGCAGCGGAGCCGAGATGGCGGCGGTTCACAAATACACCATTC 1484
QY 341 PheArgHisMetAsnTyrAspAspLeuLeuAlaTyrArgValAspProPheArgPro 360
Db 1485 TTCAAAACAGCTCACTGGGACATGTGCTGCGCAGACGCTCGAGCGGCTTAAACCG 1544
QY 361 CysLeuGlnSerGluGluAspValSerGlnPheAspThrArgPheThrArgGlnThrPro 380
Db 1545 CTCTTGAGAGAGGAGATGATGTCTTCACGTTGCGATACAGATTCAAGACAAATTCGA 1604
QY 381 ValAspSerProAspAspThrAlaLeuSerGlnSerAlaAsnGlnAlaPheLeuGlyPhe 400
Db 1605 GTGATTCCTCCGTATGATCAACAGCTTAAGCGAAAGGCCAATTAATTTCCAAAGGTTTC 1664
QY 401 ThrTyrValAlaProSerValLeuAspSerIleLysGluGlyPheSerPheGlnProLys 420
Db 1665 ACCTACGTTGCACCTCGATCTGAGGATATGCAATCGG-----GCCAAGCGATGCCA 1718
QY 421 LeuArgSerProArgArg-LeuAsnSerSerProArgValProValSer----- 436
Db 1719 GCACGCTCCCAAGCAGCACTCCACGCGCAGCTGCGGACAGAGCTTCGCGCTGCAGTTTC 1778
QY 437 -----ProLeuLysPheSerProPheGluGlyPhe----- 446
Db 1779 CCATGGCCCAATGTGGCGCCAAATGGCGCTGCGGCATGACAGCGTCAATTCGACAGATTC 1838
QY 447 -----ArgProSe 449
Db 1839 CGGAGTGTTCGACGAGCCCGCCGCGCATGCATGCAGACATTTTGGCGCGCTGCATTC 1898
QY 449 rProSerLeuProGluProThrGlu-----LeuPro-----LeuProBr 462
Db 1899 GCCGGCGCAGGACGATGATGAGCGTGCAGAGGTCTGCCGATGCTTAAAGCTGGAGCG 1958
QY 462 OLeuLeuProProProProSerThrThrAlaProLeuProIleArgPro----- 479
Db 1959 ATTGCTCCCAACCAACCAACCAATCCATCCGTCGCTCGTGCAACCCAGCAACTG 2018
QY 480 -----ProSerGlyThrLysLysSerLysArgGlyArgGlyArg 492
Db 2019 CATCAAGCTTCCTCTCCCTACCCCAAAAAAAAAAAAAAAAAAAAAAAAAACAGCAAAAG 2078
QY 492 g 492
Db 2079 A 2079
RESULT 8
ABL16561


```
QY 260 nargAlaValaAsp---TriPTrpSer-----LeuGlyAlaLeuMetYrAspMetLe 276
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 838 GCCCTTCGTGGCGCGCTGGTGGCAGGAGCTGCCGCTGGAGCCGCTGATGACACATGCT 897
QY 276 uThrGlySerProProPheThrAlaGluAsnArgLysLysThMetAspLysIleIleAr 296
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 898 CACTGGATGCGCGCCCTTTACCCAGAGAAACGGAGAAACCATGATGATCATCAG 957
QY 296 gGlyLysLeuAlaLeuProProTyrLeuThrProAspAlaArgAspLeuValLysLysPh 316
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 958 GGGCAAGCTGGAGCTACCTCCCTACTCCTACCCAGATGCCGGGAGCTTGTCAAAAAGTT 1017
QY 316 eLeuLysArgAsnProSerGlnArgIleGlyGlyProGlyAspAlaAlaAspValG1 336
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1018 TCTGAAGAGGAATCCAGCAGCGGATTTGGGGTGGCCCGAGGGATGCTGATGTGCA 1077
QY 336 nArgHisProPhePheArgHisMetAsnTrpAspAspLeuAlaTrpArgValAspPr 356
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1078 GAGACATCCCTTTTTCGGGACATGATGGAGGAGCACTTCTGGCTGGCGTGGAGCC 1137
QY 356 oProPheArgProCysLeuGlnSerGluGluAspValSerGlnPheAspThrArgPheTh 376
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1138 CCTTTCAGGCGCTGTCTGACAGTCAAGAGAGAGCGTGAAGCTTTGATACCGGCTTAC 1197
QY 376 rArgGlnThrProValAspSerProAspAspThrAlaLeuSerGluSerAlaAsnGlnAl 396
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1198 ACGGACAGAGCGCGGTGGAGAGCTCTGATGACACAGCCCTCAGGAGAGTCCAAACGAGC 1257
QY 396 aPheLeuGlyPheThrTyrValAlaProSerValLeuAspSerIleLysGluLysPhe 416
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1258 CTTTCGCGGGCTTTCACATACGTGGCGCGCTGTCTGTCGAGACATCAAGAGAGGCTTCTC 1317
QY 416 rPheGlnProLysLeuArgSerProArgArgLeuAsnSerSerProArgValProValSe 436
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1318 CTTCCAGCCCAAGCTGCGCTCACACCGCGCTCAACAGTACGCCCGGGGTCCCGCTCAG 1377
QY 436 rProLeuLysPheSerProPheGluGlyPheArgProSerProSerLeuProLupProTh 456
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1378 CCCCCTCAAGTCTCCCTTTTGGAGGGGTTTCGGCCAGCCAGCCCTGCCGAGCCAC 1437
QY 456 rGluLeuProLeuProProLeuLeuProProProProSerThrThrAlaProLeuPr 476
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1438 GGGGCTACCTTACCTCACTCTGCCACCGCGCGCTTCGACACCGCCCTCTCC 1497
QY 476 oIleArgProProSerGlyThrLysLysSerLysArgGlyArgGlyArgProGlyArg 495
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1498 CATCGCTCCCGCTCAAGGAGCAAGATCCAGAGGGGCGGTGGCGCTCCAGGGCGT 1555
RESULT 10
AA235657
ID AA235657 standard; cDNA; 1609 BP.
XX
AC AA235657;
XX
DT 26-JAN-2000 (first entry)
XX
DE Human serine/threonine protein kinase 2 encoding cDNA.
XX
KW Human; serine/threonine protein kinase; HSTK-1; HSTK-2; diagnosis;
XX cancer; inflammatory disease; growth disorder; development disorder; ss.
XX
OS Homo sapiens.
XX
XX Key location/Qualifiers
XX FH 103..1590
XX FT /tag=
XX FT /product= "serine/threonine protein kinase"
XX
XX US985635-A.
XX PN
XX PD 16-NOV-1999.
XX
```

```
PF 15-NOV-1996; 9605-0749902.
XX
XX 15-NOV-1996; 9605-0749902.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman O, Hallman JL, Goll SK;
XX
DR WPI: 2000-012793/01.
XX P-PDB: AAY49911.
XX
PT Human serine/threonine protein kinases and encoding polynucleotides for
XX diagnosis, prevention and treatment of cancer, inflammatory diseases
XX and growth and development disorders -
XX
PS Disclosure: Fig 2; 40pp; English.
XX
CC The present invention describes two human serine/threonine protein
CC kinases designated HSTK-1 and HSTK-2, which have chemical and structural
CC homology to two p70 S6 ribosomal kinases from man (GI 189508) and rabbit
CC (GI 1562), and to serine/threonine kinase from fetal liver (GI 1480861),
CC and XEEK1 (GI 1016551) from the African frog, Xenopus laevis.
CC Compositions comprising the two serine/threonine protein kinases are
CC useful for the diagnosis, prevention or treatment of cancer,
CC inflammatory diseases, and growth and development disorders. The
CC present sequence encodes HSTK-2.
XX
SQ Sequence 1609 BP; 312 A; 519 C; 472 G; 283 T; 23 other:
XX
Alignment Scores:
Pred. No.: 6,15e-85 Length: 1609
Score: 1385.50 Matches: 285
Percent Similarity: 70.65% Conservative: 40
Best Local Similarity: 61.96% Mismatches: 69
Query Match: 53,00% Indels: 67
DB: 21 Gaps: 10
XX
US-09-762-258-2 (1-495) x AA235657 (1-1609)
QY 86 LeuGlyLysGlyLysTyrGlyLysValPheGlnValArgLysValGlnGlyThrAsnLeu 105
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 229 CTGGGGAGGGCGCTCATGCGCCAGTGCAGACTGC-----ATTAACTG 273
QY 106 -----GlyLysIleGlyAlaMetLysValLeuArg-----LysAla 117
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 274 ATCACACAGCAGGAGTACNCCTGCANATCATGNTTTTTCAGAGCCACATTCGAGAG 333
QY 118 LysIleValArgAsnAlaLysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGlu 137
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 334 AGGGTTTTCAGGGAGGTGAGATGCTGTACCACTGCCAGGAGACAGAAAGTCTTAGAG 393
QY 138 SerValLysHisProPheIleValGluLeuAlaTyrAlaPheGlnThrGlyLysLeu 157
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 394 CTGATTGAGTTC-----TTGAGAGAGAGGAGCCCTTC 426
QY 158 TyrLeuIleLeuGluCysLeuSerGlyGlyLeuPheThrHisLeuGluArgGlyGly 177
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 427 TACCTGGTGTGTTGAAGAAGTACGGGAGGCTCATCTGAGCCACATCCAGAGCCGCG 486
QY 178 IlePheLeuGluAspThrAlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHis 197
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 487 CACTTCACAGAGCTGGAGGCGAGCGGTGTGTGCAGAGTGTGCCAGCGCTTGGACTTT 546
QY 198 LeuHisSerGlnGlyIleTyrArgAspLeuLysProGluAsnIleMetLeuSerSer 217
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 547 CTGCATTAACAAGGATTCGCCCCACAGGAGCTTAACCCGGAACAATCTCTGTGAGCAC 606
QY 218 GlnGlyHis-----IleLysLeuThrAspPheGlyLeu----- 228
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 607 CCCAACAGGCTCCTCCCGGAGGAAGATCTGAGACTGTGACCTGGAGCGGAGCATCAAGTC 666
QY 229 -----CysLysGluSerIleHisGluGlyAla-ValThrHisThrPheCysGlyTh 245
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Db 667 AACGGGAGCTGCTCCCTAT-CTCCACCCGAGGCTGCTCACTCCG-----TGGGGCTC 719
Oy 245 rIleGlutyrMetAlaProGluIle----- 253
Db 720 GCGGAGTACATGCCCCGAGAGTAGTGAGGCTTCAAGCAGAGGCTAGCATTTACGA 779
Oy 254 -----LeuValArgSerGlyHis 260
Db 780 CAAGGCTGCGACCTGTGAGGCTGGGGTCACTTGTATATTCACACAGGGGCTACCC 839
Oy 260 nArgAlaValasp---TTPTPser-----LeuGlyAlaLeuMetTyrAspMetIle 276
Db 840 GCCCTTCTGGGCGCGCTGGCAGCGACCTGCGGACCGCTGATGATCATCATCATC 899
Oy 276 uThGlySerProProPheThrAlaGluAsnArgIleTyrThrMetAspIleIleIleAr 296
Db 900 CACTGGATGCGCGCCCTTACCGCAGAGAACGGAAACCAAGATAGATATCATCAG 959
Oy 296 gGlyLysLeuAlaLeuProTyrLeuThrProAspAlaArgAspLeuValLysLysPh 316
Db 960 GGGCAGAGTGGACACTNCCCTTACTCACCACCCAGATCCCGGGACCTTGTCAAAAGTT 1019
Oy 316 eleuLysArgAsnProSerGlnArgIleGlyGlyProGlyAspAlaIleAspValG 336
Db 1020 TCTGAACGGAATCCACACGCGGATTTGGGGTGGCCAGGGGATGCTGATGATGCA 1079
Oy 336 nArgHisProPhePheArgHisMetAsnTrpAspAspLeuAlaIleTyrValAsp 356
Db 1080 GAGACATCCCTTTTCCGCGACATGATGGAGCACCCTTGGGCTGGCGTGGAGCC 1139
Oy 356 oProPheArgProCysLeuGlnSerGluGluAspValSerGlnPheAspThrArgPhe 376
Db 1140 CCCTTACAGGCGCTGTGCGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1199
Oy 376 rArgGlnThrProValAspSerProAspAspThrAlaLeuSerGluSerAlaAsnGln 396
Db 1200 ACGGAGAGCGCGGTGGAGAGTCTGATGACACAGCCCTCAGAGAGAGAGAGAGAG 1259
Oy 396 aPheLeuGlyPheThrTyrValAlaProSerValLeuAspSerIleLysGluGlyPhe 416
Db 1260 CTTCCTGGGCTTCACATACGTGGCGCGCTGTCTCTGGACACATCAAGAGAGGCTTC 1319
Oy 416 rPheGlnProLysLeuArgSerProArgArgLeuAsnSerSerProArgValProVal 436
Db 1320 CTTCAGGCCAACGTCGCTACCCAGGCGCTCAACAGTACCCCGGCTCCCGTCA 1379
Oy 436 rProLeuLysPheSerProPheGluGlyPheArgProSerProSerLeuProGluPro 456
Db 1380 CCCCCCAAGTTCCTCCCTTTTGAGGGGTTTCGGCCCAAGCCCTGCGGAGCCGAC 1439
Oy 456 rGluLeuProLeuProProLeuLeuProProProProProSerThrThrAlaProLeu 476
Db 1440 GAGGCTACCTACTCTCCACTCTCCACCGCGCGCCCTTGACACCGCCCTCTCC 1499
Oy 476 oIleArgProProSerGlyThrLysLysSerLysArgGlyArgGlyArgProGlyArg 495
Db 1500 CATCCGTCCTCCCTCAGGAGACCAAGATCCCAAGAGGGGCTGGGCGTCCAGGGCGT 1557

RESULT 11
ID AAK86892 standard; DNA; 6923 BP.
XX AAK86892;
AC
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41704.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytosolic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
XX

PN W0200157182-A2.
XX 09-AUG-2001.
PD 17-JAN-2001; 2001W0-0S01354.
PF
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0227182.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229347.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.

PR	29-SEP-2000	2000US-02363627
PR	29-SEP-2000	2000US-02363637
PR	29-SEP-2000	2000US-02363638
PR	29-SEP-2000	2000US-02363639
PR	29-SEP-2000	2000US-02363640
PR	02-OCT-2000	2000US-02366802
PR	02-OCT-2000	2000US-02370307
PR	02-OCT-2000	2000US-02370308
PR	02-OCT-2000	2000US-02370309
PR	02-OCT-2000	2000US-02370400
PR	13-OCT-2000	2000US-02393937
PR	13-OCT-2000	2000US-02393938
PR	20-OCT-2000	2000US-02403660
PR	20-OCT-2000	2000US-02411221
PR	20-OCT-2000	2000US-02411785
PR	20-OCT-2000	2000US-02411786
PR	20-OCT-2000	2000US-02411865
PR	20-OCT-2000	2000US-02411866
PR	20-OCT-2000	2000US-0241809
PR	20-OCT-2000	2000US-02418098
PR	20-OCT-2000	2000US-02418109
PR	01-NOV-2000	2000US-02445126
PR	08-NOV-2000	2000US-02465475
PR	08-NOV-2000	2000US-02465476
PR	08-NOV-2000	2000US-02465477
PR	08-NOV-2000	2000US-02465478
PR	08-NOV-2000	2000US-02465523
PR	08-NOV-2000	2000US-02465524
PR	08-NOV-2000	2000US-02465525
PR	08-NOV-2000	2000US-02465526
PR	08-NOV-2000	2000US-02465527
PR	08-NOV-2000	2000US-02465528
PR	08-NOV-2000	2000US-02465532
PR	08-NOV-2000	2000US-02465532
PR	08-NOV-2000	2000US-02465609
PR	08-NOV-2000	2000US-02465610
PR	08-NOV-2000	2000US-02466513
PR	17-NOV-2000	2000US-02492912
PR	17-NOV-2000	2000US-02492913
PR	17-NOV-2000	2000US-02492914
PR	17-NOV-2000	2000US-02492915
PR	17-NOV-2000	2000US-02492916
PR	17-NOV-2000	2000US-02492917
PR	17-NOV-2000	2000US-02492918
PR	17-NOV-2000	2000US-02492924
PR	17-NOV-2000	2000US-02492925
PR	17-NOV-2000	2000US-02492926
PR	17-NOV-2000	2000US-02492927
PR	17-NOV-2000	2000US-02492929
PR	17-NOV-2000	2000US-02493000
PR	01-DEC-2000	2000US-02503160
PR	01-DEC-2000	2000US-02503191
PR	05-DEC-2000	2000US-02510330
PR	05-DEC-2000	2000US-02510388
PR	05-DEC-2000	2000US-02516719
PR	06-DEC-2000	2000US-02516799
PR	06-DEC-2000	2000US-02516856
PR	08-DEC-2000	2000US-02516868
PR	08-DEC-2000	2000US-02516869
PR	08-DEC-2000	2000US-02516899
PR	11-DEC-2000	2000US-02545937
PR	05-JAN-2001	2001US-02559678
XX		
DA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
XX	Rosen CA, Barash SC, Ruben SM,	

XX	WPI: 2001-483426/52.
XX	
PR	Nucleic acids encoding human immune/hematopoietic antigen polypeptide
PT	useful for preventing, diagnosing and/or treating cancers and
PT	metastasis -
XX	
PS	Disclosure; SEQ ID NO 41704; 3071bp + Sequence Listing; English.
XX	
CC	AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (
CC	amino acid sequences given in AAM82170 to AAM91921. (I) have cytostat
CC	activity, and can be used in gene therapy and vaccine production. (I)
CC	proteins and polynucleotides may be used in the prevention, diagnosis
CC	treatment of diseases associated with inappropriate (I) expression. F
CC	example, they may be used to treat disorders associated with decreased
CC	expression by rectifying mutations or deletions in a patient's genome
CC	that affect the activity of (I) by expressing inactive proteins or to
CC	supplement the patients own production of (I). Additionally, (I)
CC	polynucleotides may be used to produce the secreted (I), by inserting
CC	the nucleic acids into a host cell and culturing the cell to express
CC	protein. (I) proteins and polynucleotides may be used to prevent,
CC	diagnose and treat immune/haematopoietic-related diseases, especially
CC	cancers and cancer metastases of haematopoietic-derived cells. AAK647
CC	to AAK87694 represent human immune/haematopoietic antigen genomic
CC	sequences from the present invention. AAK54942 to AAK54950 and AAM821
CC	represent sequences used in the exemplification of the present invent
XX	
SQ	Sequence 6923 BP; 1252 A; 2025 C; 2044 G; 1602 T; 0 other:
	Alignment Scores:
Pred. No.:	4,66e-84 Length: 6923
Score:	1383.00 Matches: 486
Percent Similarity:	21.86% Conservative: 0
Best Local Similarity:	21.86% Mismatches: 6
Query Match:	52.91% Indels: 1755
DB:	Gaps: 14
US-09-762-258-2 (1-495) x AAK86892 (1-6923)	
OY	4 GYARGATGALAAAGGLYALAAGLYAALAAmetaLAAlaVAlpheaspleuAspleuglu 23
Dd	
	31 GGCGCAGGGGCCCGGGGGCGGGCGGCACATGGCGGCGGTGGATTGGATTTGGAG 90
OY	24 ThrGlutgluLysSerGIuGLyGIuGLyGIuProGIuLeuSerProAla----- 39
Dd	91 ACGGGAAGAAGCAGAGGAGGCGAGGCGAGCACAGCTCAACCOCGGCGTAGTGCCCTG 150
OY	39 ----- 39
Dd	151 CCCTGGCCGCACTGGATTCCTGGAGCCCATCTGTACACCAGCCGAGGCCGAGCGCGC 210
OY	39 ----- 39
Dd	211 TCCCGACGCCAGAGCGGGCTCCGACTCTTTCAGAACCCAGATCCTTCAGATCCGGT 270
OY	39 ----- 39
Dd	271 CTCATTAAGTTCTGATCCACCTCAACCCGACCTCTCTTCCAAGAACCCAGACCTTTTC 330
OY	39 ----- 39
Dd	331 TCCCGATTCCTCCCTTTCTCTGCGTTCTCGGTTCTTTCCAAATTCTTAACCATCCCTACTAGC 390
OY	39 ----- 39
Dd	391 TGCCATCCCTGACACACCTTCTCTCTCGGCGACGACAGTCCAACTGAACGGAGCGGGA 450
OY	40 ----- AsplacySProle 44
Dd	451 GGTATCCCTGGCACTTCCTTGCTCTTAACCCCTCGGTTTTCTCACAGGACGATGCCCCCT 510
OY	44 uAlaGIuLeuARgAlaAlaagLyLeuGIu----- 53

Db 511 TCCGAGTTGAGGCGCTGGCCTAGAGTGAAGGTCTGTTGGGGAGGGGGAAT 570
QY 53 ----- 53
Db 571 GGAGTGGGAAGGGAGACTGGGAGCCTGGAGCCTTGCTCATTAACCTCTGTGTC 630
QY 54 ----- ProValGlyHisTyrGluValGluLeuThrGluuHisSerValAsnValGlyP 72
631 GTAGCCTGTGGACACTGTAAGAGGTGAGCTGACTGAGACAGCGTAAGCTTGGCC 690
QY 72 TGGTAATGAGGlyProHisCysPheGluLeuLeuArgValLeuGlyLysGlyTyrG 92
691 CAGACCGATCGGGCCCACTGTTGAGCTGCTGCTGGGCAAGGGGGCTATG 750
QY 92 Llys----- 93
Db 751 GCAAGGTAGGGGGGGCGGCGACCTCTCTGGCCTCACAGCCTCCATCTGGAGGACAA 810
QY 93 ----- 93
Db 811 AGGTTCTCAAAACAATAATAGACTTGTGAATCAGCAGGCGCTATAGGATTCAGAGCC 870
QY 93 ----- 93
Db 871 AGAAACATAAAGAGGAGGAGGCCAAATCCTTCATCGACTGAAATCTTCACTGCC 930
QY 93 ----- 93
Db 931 CACCTTGGCAGGGCCTAGGCCCTCTGATCCCAAGCCAGACCTTCAGGGTGGGCTTCT 990
QY 94 ----- ValPheGln 96
Db 991 TGAAGATAGATGTGAGAGGGAAGTGTGATCCTGCTCCCTGCCCCCTACAGGTGCCAG 1050
QY 97 ValAlaGlyValAlaGlnGlyThrAsnLeuGlyLysIleTyrAlaMetLysValLeuArgLys 116
1051 GGGCAAAAGGTGCAAGGCCAACCACTTGGGCAAAATATATGCAATGAAGTCTCTAAGGAAG 1110
QY 117 Ala----- 117
Db 1111 GT-GAGTCACTGCTTCAGCCAAAGAACTACTGTGGCTGCCATTCGCCAACATGCTGTACC 1169
QY 117 ----- 117
Db 1170 AGGTTTGGGAAGACAGCAGGAGACACAGTGGAGAGATCCCTGACTTGGCGTTGCT 1229
QY 117 ----- 117
Db 1230 GGTATATGTCTGTGTGTGATGTGTAATGTCTTGCAGTAATTCATGGGGCAATTGG 1289
QY 117 ----- 117
Db 1290 ACTCCAGCAGACATTTGACAAACAGTGTCTGCACACTATTTATTTTATTTTAAAG 1349
QY 117 ----- 117
Db 1350 ACGGAGTCTTGTCTGTGTACCCAGGCTGAGTGCAGTGCAGGATTTTGGCTACAGCCA 1409
QY 117 ----- 117
Db 1410 CCTCTGTCTCCAGGTTCAAGCAGATCTGCTGCTAGACTCCGAGTAGCTGGGATAC 1469
QY 117 ----- 117
Db 1470 AGGCGCTGGCACACACCCAGCTAATTTTGTACTTTTGTAGAGGTGGGTTTCGCC 1529
QY 117 ----- 117
Db 1530 TGGCTGTCTTAAGTCTAATCTCAGGTATCTGCCGCTTGGCTCCAAAGTGTCTGG 1589
QY 117 ----- 117
Db 1590 GAGCTGGGATTACAGGCAATGAGCACCGTCCCTAGCTTTTATTTTATTTTGGATGAGTTC 1649

QY 117 ----- 117
Db 1650 TTGCTTTGTTCCCGACACTGAGTGCAGTAGTGCACTCTCTGCTACATGCAACTCTGCC 1709
QY 117 ----- 117
Db 1710 TCCCGGTTCAAGTAATTCCTTACTCAGACCTCTGAGTAGTGTGGACTACAGGCTGTG 1769
QY 117 ----- 117
Db 1770 GGCACACACCTGGCTAATCTTGTATTTCTATTTGTTTACTACTTATTTTGAGACGA 1829
QY 117 ----- 117
Db 1830 GTCTCACTGTGCACACGCTGAGAGTGCAGTGTGCGATCTGCGCTCACAGCAACTTC 1889
QY 117 ----- 117
Db 1890 CACCTCCAGGTTGAAGTATTCCTCTGCTCAGCCTCCTGAGTAGCTGGATTCAGAGC 1949
QY 117 ----- 117
Db 1950 GTGAACCACTACTCTGCTAATTTTTTTTTTTTGTATTTTATAGAGATGGGTTTTTG 2009
QY 117 ----- 117
Db 2010 TCATGTGTGACAGCTGTGTCTTGAACCTCCTGACCTCAGGCTATCCGCTACCTTGGCTTC 2069
QY 117 ----- 117
Db 2070 CCAAAGTGTGGGATTACAGCATGAACACACCGTGCCTGAGTTTGTACTTTTAA 2129
QY 117 ----- 117
Db 2130 GTGGAGCAGGGTTCACCATGTGTGTGAGGCTGTCTGAACCTCTGACCTCAGGTGAT 2189
QY 117 ----- 117
Db 2190 TCGCTGCTCAACCTCCCAAAAGTCTGGGATTACAGTGTGATCCACTGCGCTGGCAT 2249
QY 117 ----- 117
Db 2250 GGCACATTTTGTATGTCAAGCAGAGGGAGTGTACTGGCACCCGGTGGGTGAGA 2309
QY 117 ----- 117
Db 2310 CCAAGGATGCTGTGAACATCCACGATGCGCAGGCGACCTCCCAACAAAGATGAC 2369
QY 117 ----- 117
Db 2370 CTGGTCCAGGTGTCAGTAGTGTGCCGAGGTTGAGAAACCTGTGTGTAGAGATTAACCCAT 2429
QY 117 ----- 117
Db 2430 CCCTGAAATGATGTTGGTGTGACAGCAGCAGATATATGAGAAATACATGCAGTGACAG 2489
QY 117 ----- 117
Db 2490 AGGATGCACAGTTAACAACAGATGATGCTGAGAGACTCTGGTGCCTCCCATTTT 2549
QY 117 ----- 117
Db 2550 TTTTTTTTTTTTTTTTGAAGTAGTGTCTGCTCTGTACCCAGGCTGGAGTGCAGTGGC 2609
QY 117 ----- 117
Db 2610 GTGATCTCAGTCACTGCAACCTGTGCCCTGGGTTCAAGCAGATCTCTGCTCAGCCT 2669
QY 117 ----- 117
Db 2670 CCTGAGCTGGGATTACAGCGGTGTACCATCATACCAGCTAATTTTCTATTTTATAGTAG 2729

OY	117	-----	117
Db	2730	AGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAAATTCGTGACCTCAGGTAATCCG	2789
OY	117	-----	117
Db	2790	CTGCCTTGGCCTCCTACAGTGTGGATTACAGGTGTGAGCCACATGTGCCAGCTGGAT	2849
OY	118	-----	125
Db	2850	GCCTCAGTTTCTAACCAATTCTGTATCTCAGAGCCAAAATTTGGGCAATGCCAAGAC	2909
OY	126	Thra1aHstHra1aGla1aGAsn1Leu1eGluSerVal1yHs1ProPhel1eVal	145
Db	2910	ACAGCACACACACGCGCTGAGCGGAACATTCTGAGTCAGTGAACACCCCTTATTTGTG	2969
OY	146	Glu1eua1aTy1ra1aPheG1nThrg1yG1y1yLeu1Ty1Leu1Leu1eGlu1y1euser	165
Db	2970	GAACCTGGCCTATGCTCTCCAGACTGGTGGCAAACTTACCTCATCTTGTAGTGCCTCAGT	3029
OY	165	-----	165
Db	3030	GGTATGATGCGGCGGCCACAGCAGGGGGTCTGGGGGTCTCGCGGGGGGGCAGCAGCA	3089
OY	165	-----	165
Db	3090	AGGAAGCTTGGGGGGAAGCTCTTGAGAGATGATGTGTGGGGGTGTGGCTAGGGGGCCC	3149
OY	165	-----	165
Db	3150	CACCTGTGCTACCCATCCATCCATCCATCCGTCGATCCGTCGCATCTTCATTCA	3209
OY	165	-----	165
Db	3210	GCAAAAGCTGTCCAGACCTACTGTGTCCCTCAGCTGTGTGGGGGTGATGGGCATGG	3269
OY	165	-----	165
Db	3270	TGCGAATTGGATAGAAAGTCCAGAGATGGTGAATCTCTCTACTCCCTCCTGTCT	3329
OY	165	-----	165
Db	3330	TGTTCTTCTCTCCGCTGTGCGCTGTGCAATCCGTGAGGTCCCCAGCCCACTGTTATTCT	3389
OY	165	-----	165
Db	3390	CTGTAGTCTCTCTCCATCCGTTCACATCTCAGGGGCTGTGGGGTGGCAGACACTT	3449
OY	165	-----	165
Db	3450	TTTAACTGGGCTGAGGCTCCGCGTCACTGCTTCTGTGTCTCTGTGCCAGTCT	3509
OY	165	-----	165
Db	3510	GAGGTCAATAGAGCTGGGGCTGCTCCAGCCCTTCTATTACAGATCTGGGCTGGCTGC	3569
OY	165	-----	165
Db	3570	CCACATCAAGCCTTGCCCTTAGGGCGGCTGTCCCTGCAAGGCTGTGAGCAGTCTTGACT	3629
OY	165	-----	165
Db	3630	GCCTTTCCCTCGTTTGGGCGAGATGAACCTGCGAAGCTTCTGCCATCATGCTGCATTC	3689
OY	165	-----	165
Db	3690	GCTCCGTCCATCTCAGCATCCCTTAAAGTCCAGCAAAACGCGCTTCTCTGTCTGT	3749
OY	165	-----	165
Db	3750	CTGTGGGATTCACCTGTGTCTTCCCTGTCTTCTCTCGAGATCTTTTGGGCTAAAGCTTT	3809
OY	165	-----	165

Db	3810	GGAGCTGTGGCCTTGCCCTGGCCGCTTATAGAGCCGTTGTGTACATGCTCTGTCCCCAGTA	3865
QY	165	-----	165
Db	3870	GACTGAGCGTCTCATTAGGGCAGATGGCTGGCTCTTCATCTCTGCCCCACACTTCACCCAGC	3925
QY	165	-----	165
Db	3930	ACAGGGCCAGGACCGAGTAGGGCTCGTAGATGTTTGTGAAATTGAAATTGAATCCGAC	3985
QY	165	-----	165
Db	3990	GCGACGCTGTGTAGGCGAGGTAGGGCGGGAATTATGAGCCCTCTTTCCCAAGAAAGAAAT	4045
QY	165	-----	165
Db	4050	AAAGACTCAGAAACACAAAGGGGGCTTGACCCAGACAGTGGGTGTGACGTGTGTGT	4105
QY	166	----GlyGlyGluLeuPheThrHisLeuGluAlaArgGlyIlePheLeuGluAspThrAla	184
Db	4110	GCGAGGTGGCGAGGCTCTTTCACGCACTGAGCGAGAGGGGCACTCTCTGGAAGATAGCGC	4165
QY	184	a-----	184
Db	4170	CTGCGGGGTGTATTCCTCCGCTTTCCTGAGGCTGGCAGGTCCCTGCTCTACTCCGGCT	4225
QY	185	-----CysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisL	198
Db	4230	TCACCTGCTCTTGTCTTCTGCGAGCTTACCTGGCTAGATACAGGCTGGGCTGGGCGCATC	4285
QY	198	euhHisSerGlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerG	218
Db	4290	TCCACTCCCAAGGCGCATATCTACCGGAGCCTCAAGCCCGAAGAACATATGCTCAGCAGCC	4345
QY	218	1n-----	218
Db	4350	AGGGTGGCATGTGTGTGCGGGCAGTGCAGCGGGGGTCTGCAACTGTGGGAGAGGCTG	4405
QY	219	-----GlyH	220
Db	4410	AGGACCTCTGTGGGTGGGGGTGGGCGCTGGTACAGGCTCTCCAAACCCCTCTCAGAGCC	4465
QY	220	IsIleLysLeuThrAspPheGlyLeuCysLysGluSerIleHisGluGlyAlaValThrH	240
Db	4470	ACATCAAACTACCGGACTTTTGGACTCTGCAGAAGAGTCTATCCATTGAGGGCGCGTCACTC	4525
QY	240	IsThrPheCysGlyThrIleGluTyrMetAla-----	250
Db	4530	ACACCTTCTGGCGACCATTTGAGTACATGTGA-AGTGGACACTGGCTGGCCAGGGGTGCG	4585
QY	251	-----Prog	252
Db	4589	GAGGACACCCGAAAGGGGACAGGGCTGTGACTGCAGATTTCCACTCGACCCAGGCGCCCTTG	4645
QY	252	IuIleLeuValArgSerGlyHisAsnArgAlaValAspTyrPsrLeuGlyAlaLeuM	272
Db	4649	AGATTCTGTGTGCGAAGTGGCCACACACCGGCGCTGTGACTGTGTGAGACCTTGGGGGCCGTGA	4705
QY	272	eTyrAspMetLeuThrGlySer-----	279
Db	4709	TGTACGACATCTCACTGATCGCAAAAGTCCAGCCCGGGGAGAGAGAGGGGAGGGGC	4765
QY	279	-----	279
Db	4789	AGAGGTGGAGTAGCCCCCTCTGTGGGGCAAGGGGCGTGTGTGGAGGCCACAAAG	4825
QY	280	-----ProPheThrAlaGluAsnArgLysLysThrM	291
Db	4829	CTCCCTCACCCTTATATATCTCTCCAGCGCGCCCTTTCACCCAGAGAAACGGAAGAAACCA	4885
QY	291	eTasPysIleIleIleArgGlyLysLeuAlaLeuProTyrLeuThrProAspAlaArgA	311

Db 4889 TGGATTAAGATCATACAGGGGCAAGCTGGACCTGCCCCCTACTCACCCCAAGATGCCCCGGG 4948
QY 311 sPLeuValLysLys----- 315
Db 4949 ACCTTGTCAAAAAAGGTGGACGCTCCCTTCTCTCTCTCCGGGGCCCTGCCAGCCATTCTGC 5008
QY 315 ----- 315
Db 5009 ACCTGTCCTGAGTCTCTCTGGGCTGTGGGAAGCAGGGCCACCCGGCCTGTGCAGTT 5068
QY 315 ----- 315
Db 5069 TGCCTCTGGGAATGAAGAGGCCCTCCCTTGAAGTCAGAGGATTGAGCCAGGCTCAGC 5128
QY 315 ----- 315
Db 5129 CCTGTACAGACAGCAGCTGCTGCCCTTGCCCCAGTCTTAGGCTGAGTCTTAACCAAGTGACA 5188
QY 315 ----- 315
Db 5189 GCCTGTGATGAGTGTGCCACACTTCCGTCAAGGGAGCATCGAGGTGTTAGGGGGAG 5248
QY 315 ----- 315
Db 5249 GCGGACACACACATGAGGGAGTTGGCCCTCAACAAGCCCTGGGGCAATGCCAGGC 5308
QY 315 ----- 315
Db 5309 CCAGGAGCCTCTGCAAAAGCCTTTGTGAGAGGTGGCTCATTGACCAAAACCTTGAAAGC 5368
QY 315 ----- 315
Db 5369 CCTGAGGATATCCATAGTGGGAGCCACACCCAAAAGCATTTCTTCCATGTCCACTGAC 5428
QY 315 ----- 315
Db 5429 CCTACTCCAGCTAGCCCTGGAGACCCGGGACACATGACGACTTGGCCAGGCCCTCA 5488
QY 316 ----- 315
Db 5489 CCCTCTCTCTGCTGCCCGGAGTTTCTGAAACGGAAATCCAGCGGAGATTGGGGTGGC 5548
QY 329 ProGlyAspAlaLysPval----- 335
Db 5549 CCAGGGGATGTCTGATGTGT- GCAGGTGGGTTTGGGACCAACCAAGGGGTAGGGCTGAG 5607
QY 335 ----- 335
Db 5608 TCTCCAAAGGTGCCGGGAATGGGGGAGGGGCCCAAGGAGAGGAGTGCAGCGGGGCA 5667
QY 336 ----- 341
Db 5668 AGCAGGGTACGCTGTAGTGGGTTTGGTCAATTTCTTACCTACAGACATCCCTTTTTC 5727
QY 342 ArgHisMetAsnTyrPaspLeuLeuAlaTyrPargValAspProPheArgProCys 361
Db 5728 CGGACATGAATTTGGAGACACCTTCTGCGCTGGCGTGTGACCCCTTTAGAGCCCTGT 5787
QY 362 Leu----- 362
Db 5788 CT- GGTGACAGCAGGGCTGTGGCCAGTGGCCGCTGGCGGTGGCAAGTGGAGAACTTG 5846
QY 363 ----- 367
Db 5847 CATCTTGGTCCCTTGACCCCTCCCTCACTGTGGTGGCCACAGAGTCAAGAGGAGGC 5906
QY 368 ValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSerProAspPheThr 387
Db 5907 GTGAGCACTTTGATACCGGCTTCAACAGGAGAGCCGGTGGACGTCTCTGATGACACA 5966
QY 388 AlaLeuSerGlnSerAlaAsnGlnAlaPheLeu----- 398
Db 5967 GCCCTCAGGAGAGTGGCAACAGGCGCTTCTGTGAGTGGCGGGGCTGTAGGCTGTGG 6026

QY 398 ----- 398
Db 6027 GACCAAGGACGAGATGCTACTAAGATGAGGACACTGAGTGTCCGATGGCCCTGC 6086
QY 399 -----GlyPheThrTyrValAlaProSerValLeuAspSerIleLysGlnLysPhe 415
Db 6087 CGCCCCCAGGGCTTCACTATACGTGGCGGCTGTGTCTGTGACAGCATCAAGAGAGGGCTT 6146
QY 415 eSerPheGlnProLysLeuArgSerProArgArgLeuAsnSerSerProArgValProVa 435
Db 6147 CTCTTTCAGCCCAAGACTCGCTCACCAGGCGCTTCAACAGTAGCCCGCGGCCCTGT 6206
QY 435 1----- 435
Db 6207 CAGTACTGAGGAGCTGGGGGTGTGTGGCTGGGTTAGGAGCCTGGCAGGACGATGCC 6266
QY 435 ----- 435
Db 6267 AGCTCCAGCCTTGGGTGCTTGGCCACGTCGTGCGGCAAGTGTGGCTTCGGTTGCTGTG 6326
QY 435 ----- 435
Db 6327 TCTATCATGGGAGCTCAGTTCCTTACACCCCTTGTGGCCAGGCTGCTGGATGGAGTTT 6386
QY 435 ----- 435
Db 6387 GTTGAGCCCGCGGCTGTGTGCTGGGCAAGTGGGAAGGCTGCTTCCCTGACTGATG 6446
QY 436 -----SerPr 437
Db 6447 CTGGAGCCTCTGGGAGGCGCTAGAGGCTTATTCTGCTTGTTCCTCCCTGCAGGCC 6506
QY 437 OleuLysPheSerProPheGlnLysPheArgProSerProSerLeuProGlnProThrGln 457
Db 6507 CCTCAAGTCTCCCTTGTGAGGGGTTTGGCCAGCCCAAGCCTGCCGAGGCCACGGA 6566
QY 457 uLeuProLeuProProLeuLeuProProProProSerThrAlaProLeuProIle 477
Db 6567 GCTACCTTCACTCCACTCTGTGCCACGCGCGCCCTGTGACCAACGCGCCCTTCCCAT 6626
QY 477 eArgProProSerGlyThrLysLysSerLysArgGlyArgProGlyArg 495
Db 6627 CCGTCCCGCTCAGGAGCAAGATGCCAAGAGGGGCGGTGGGCGCCAGGGGCGC 6681
RESULT 12
AAK86891
ID AAK86891 standard; DNA; 4357 BP.
AC AAK86891;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41703.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
XX
XX WO200157182-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 05-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236882.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.

PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
XX PA
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483426/52.
XX DR
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX PS
XX Disclosure; SEQ ID NO 41703; 3071pp + Sequence listing; English.
XX AA554951 to AA64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AA682170 to AA691921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and

CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK67694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK62169
 CC represent sequences used in the exemplification of the present invention.
 CC
 XX Sequence 4357 Bp: 746 A; 1337 C; 1330 G; 944 T; 0 other;

Alignment Scores:

Pred. No.:	2,26e-81	Length:	4357
Score:	1340.00	Matches:	375
Percent Similarity:	29.58%	Conservative:	1
Best Local Similarity:	29.50%	Mismatches:	4
Query Match:	51.26%	Indels:	894
DB:	22	Gaps:	10

US-09-762-258-2 (1-495) x AAK86891 (1-4357)

QY 116 LysAlaIyLleValArgAsnAlaLysAspThrAlaHisThrArgAlaGluArgAsnIle 135
 Db ::
 Db 314 CAGGGCCAAATTTGTGCGCATGCGCAAGACACACACACAGCGGCTGAGGGAACATT 373
 QY 136 LeuGluSerValIyHisProPheIleValIleuAlaTyAlAPheGlnThrGlyGly 155
 Db 374 CTAGAGTCAGTGAACACACCCCTTATGTGGAAGTGGCTATGCGCTCCAGACTGTGGC 433
 QY 136 LysLeuTyLleuIleLeuGluCysIleuSer----- 165
 Db ::
 Db 434 AAACCTACCTCATCTCTGAGTGCCTCAGTGTATGAGTGCAGGCGCCAGCAGGGGTGCT 493
 QY 165 ----- 165
 Db 494 GGGGTCGGGGGGGGGCGACGACGACGAAAGAAAGCTGTGGGGGGAAGCTTTGAGAGA 553
 QY 165 ----- 165
 Db 554 TGAGTCTGGGGGTTGGCTAGGGGGCCCCCACTGTGTCTACCATTCATCCATCCATC 613
 QY 165 ----- 165
 Db 614 CGTGATCCGTCATTCATTCATTCATTCAGCAAAAGTGTGCAGCAGCTACTGTGTCC 673
 QY 165 ----- 165
 Db 674 CTCACGTGTGTGGGGGTGAGTGGCAGTGGCAATTGGATAGAAATCCAGAGAGATGG 733
 QY 165 ----- 165
 Db 734 TTGAGTCTTCTCTACTCCCTCCCTGTCTTCTCTCTCTCCGCTGCTGCATCTCT 793
 QY 165 ----- 165
 Db 794 GTGAGTCCCGCAGCCCACTGGTTCATTCCTGTAGTGTCTCTCCATCCGCTCCACTCT 853
 QY 165 ----- 165
 Db 854 CAGGGGCTGTGGGGTGGCCAGAGCACTTTCTAACTGGGTGAGGCTCCCGCTCACC 913
 QY 165 ----- 165
 Db 914 TGCCTTTAGTGTCTCTCTGCGACTGCTGAGGTATAGAGGCTGGGGCTGTCTCCAGC 973
 QY 165 ----- 165
 Db 974 CCTCTATTTCAGAGTCTCTGGGCTGGCTGCCACATCAAGCCTTGCCCTAGGCGGGCTG 1033

QY 165 ----- 165
 Db 1034 TCCCTCGACAGCTGTGAGCAGTCTTGACCTGCTTTCCTCGTTGGGCCAGATGAAACC 1093
 QY 165 ----- 165
 Db 1094 TGGAGCTTCTGCTCCATCCATGCTGTGATTCGGCTCGCTCATCTCAGCATCCCTTAAACT 1153
 QY 165 ----- 165
 Db 1154 CCCAGCAAAACCGCGCTTCTCTGTTCTGTATGTGGATTCAGTCTGTCTCCCTGCT 1213
 QY 165 ----- 165
 Db 1214 TCTCTGCGAGATCTTTTGGGCTAAGCTCTTGAGACTGTGCGCTGGGCTGGGCTATTAGA 1273
 QY 165 ----- 165
 Db 1274 GCGGTTGTATACATGTCTGTCTCCAGTAAAGACTAGAGCTGCGGAGGCGAGTGGGT 1333
 QY 165 ----- 165
 Db 1334 CTCTTCATCTGTCTCCAGCTTCCACAGCAGAGGCGCAGCAGAGTAAAGCGTCTGTA 1393
 QY 165 ----- 165
 Db 1394 GATGTTTGTCTGAATTGAATTGAATCCCAAGCGAGCTGTGAGGCGAGGTAGGGCGGGA 1453
 QY 165 ----- 165
 Db 1454 TTATAGGCCCTTTTCCCAAGAAATTAAGACTCAGAAAGCAAAAGGGGCTTGA 1513
 QY 166 ----- 174
 Db 1514 CCCAGACGTGCGCTGTGACGTGTTGTGTGCGAGGTGCGAGCTTCTACCATCTGGA 1573
 QY 174 UARGGluGlyIlePheLeuGluAspThrAla----- 184
 Db ::
 Db 1574 GCGAGAGGCACTTCTCTGGAAGATACGGCTGTGGTGTAACTCCCTTCTCTCA 1633
 QY 185 ----- 188
 Db 1634 GGCTGACAGTCCCTGTCTACTCCCGCTTACCCCTGTCTGTCTGTCTGACAGTTCTAC 1693
 QY 188 euAlaGluIleThrIleuAlaLeuGlyHisLeuHisSerGlnGlyIleIleTyArgAsp 208
 Db ::
 Db 1694 TGGCTGAGATCAACGCTGGGCTGGGCGCATCTCCATCCAGGGCAATCACTACCGGACC 1753
 QY 208 euLysProGluAsnIleMetLeuSerSerGln----- 218
 Db ::
 Db 1754 TCAAGCCGAGAACATCATGTCTCAGCAGCAGAGGTGCGCATGTGTGTGCGGCGAGCTGCA 1813
 QY 218 ----- 218
 Db 1814 GCGGGGCTGCAATCTGTGGGAGGCGTGAAGACCTGTGGGTGGGGGCGCCCTGG 1873
 QY 219 ----- 230
 Db 1874 TCACGCTCTCCAAACACCTTCTCAGGCGCAATCAAACTGACCGACTTGGACTCTGCA 1933
 QY 230 yagIuSerIleHisGluGlyAlaValThrHisThrPheCysGlyTrpIleGlyTyrMet 250
 Db ::
 Db 1934 AGAGTCTATCCATGAGGCGCGGTACTACACCTTGTGGCACCATTGATGATCATGT 1993
 QY 250 1a----- 250
 Db 1994 A-AGTGCACATGGCTGGCCAGGCTTGGGAGGAGCAGCCGAAGGGGCGAGCCTGACT 2052
 QY 251 ----- 262
 Db 2053 GACAGTTCACCTGAGACCCAGGCGCCCTGAGATTCCTGTGTGCGCACTGCGCACAAACGGG 2112

QY	262	laVaIaPTrPTpSPserLeuGIyAlaLeuMeTyTrsPheLeuThProGlySer-----	279
Db	2113	CTGTGGACTGGTGGAGCCTTGGGGCCCTGATGTACACATGCTCACTGGATCGCAATGC	217
QY	279	-----	279
Db	2173	CAGCCCCGGGGAGAGAGAGGAGGCGAGAGGGGAGAGGAGTGGGAGTAAAGCCCTCTCGGGGCA	223
QY	280	-----	281
Db	2233	AGGGCGGGGCTGGTGGAGGCCCCACAAGGCCTCTCTCACTTCCCTCTCCAGCCGCG	229
QY	281	roPheThrAlaGluAsnArgLysLysThrMetAspLysLleLeuArgLysLeuAlaL	301
Db	2293	CTTTCACCGCAGAGAACCGGAAAPAAAACCTGGATTAATCATCAAGGGCAAGCTGGAC	235
QY	301	eupProTyTrLeuThrProAspAlaArgAspLeuAlaLysLys-----	315
Db	2353	TGCCCCCTACCTACACCCCAAGATGCCGGGACCTTGTCAAAAAAGGTGACGCTCCCTCTC	241
QY	315	-----	315
Db	2413	TCTTCTCCGGGGCCCTGCAGACCATTTCTGCAGCTGTCTTCTGAATCTCTGGGCTGTGGG	247
QY	315	-----	315
Db	2473	GAAAGCAGGGCCATCCCGGCCCTGTGCAGTTTGGCTTGGAAATGAAGAAGCCCTCCCT	253
QY	315	-----	315
Db	2533	TGAAGTCAGGGATTGAAGCCCAAGCTTCAGCCCTGTCAAGACAGCAGCTGCTGCCCTGGCC	259
QY	315	-----	315
Db	2593	AGTCCTTAGGCTGAGTCTTAACCAAGTGACACGCTGTGTATGAGCTGGCCACACTTCCGTC	265
QY	315	-----	315
Db	2653	AAAGCGAGCATCGAGAGTGTAGGGGGAGGCGGACAGCCACATGGGGATTTGGCGCCT	271
QY	315	-----	315
Db	2713	CACCAACGCGCCCTGGGGCAATGCCAGGGCCCAAGAGCCTCTGCAAAGCCTTTGTGAGA	277
QY	315	-----	315
Db	2773	AGGTGGCTCATTTGACCAAACTTGAAGGCGCTGAGGGATTCATCATGATGAGGAGCCACAC	283
QY	315	-----	315
Db	2833	CAAAAGCATTTCTCCCATGTACACTGACCTGACCTACTCCAGCTAGCCCTGGAGCCGGGG	289
QY	316	-----	318
Db	2893	ACACATGAGCACTACTTGGCCAGGCCCTCACCTCTCTCTGTGCCGAGTTCTTGAAA	295
QY	319	ArgAsnProSerGlnArgLleGlyLysLysProGlyAspAlaAlaLysPyl-----	335
Db	2993	CGGAATCCCAAGCCAGCGGATTTGGGGGTGGCCCAAGGGGATGCTGCTGATGT- GCAGTGGG	301
QY	335	-----	335
Db	3012	TTTTGGACACACACAGGGGTAGGGCTGAGTCTCAAGGGTGGCCGGAAATGGGGGACAGG	307
QY	335	-----	335
Db	3072	CCCCAGGGCAGAGGGAGTGAACCGGGGGGCAAGCAGGGGTAGCTGTTAAGTGGGTTTGGTGC	313
QY	336	-----	351
Db	3132	ATTCTCTACTACAGAGACATCTCCCTTTTTCGGGACATGAAATTTGGGACGACTTCTGGCC	319
QY	352	TTPArgValasPProPheArgProCysLeu-----	362

D	b	3192	TTGGGGTGTGGACCCCTTTTCAGGGCCTGTCT- ggtgagcaccagaggcgtggtgccaatg	3250
O	y	362	-----	362
D	b	3251	gccggtgacgggtggcaatgtagaacttcatacttgggtccctgcagaccctcccaact	3310
O	y	363	-----glnsergluglaspvalserglphaspthrtrarghethrarg	377
D	b	3311	ctgtgcgcccacacagcagtgtagagagagacgtgacgcatttgatracccgcttcacacgg	3370
O	y	378	glnthrprovalaspserproaspthrAlaleuSerGIuSerAlaasnInlaPhe	397
D	b	3371	cagacgccgggtgacagctcctgatgacacagccctcagcgaagtrccacacagaccttc	3430
O	y	398	Leu-----	398
D	b	3431	ctgtgtgagtgccggggcccttagagcctgtgggacacagcagcgatcgtactaagatgg	3490
O	y	399	-----glypethrtyvalAlaPr	405
D	b	3491	cagcagctgagtggtgcgatggcccttcaccaccccccagggccttcacattagctggccgc	3550
O	y	405	oSerValleuaspserrlleygluglPheSerPhegluProlysluarSerProAr	425
D	b	3551	gtctgtccttgagcagcattcaagagagagccttctcttccagcccaagctgcctcaccag	3610
O	y	425	gArLeuAasnserserProArValProAl-----	435
D	b	3611	gcgcctcACaCAGtAgTAgCCCCCGGGGCTCCCGtCAgAGtACTAGGAGAGTGGGGGTGTGTGC	3670
O	y	435	-----	435
D	b	3671	ttgggttagggacgtgcgacagcagatgcacgtccagccttgggtgcttggccacacgtc	3730
O	y	435	-----	435
D	b	3731	ttgtgcgcagatgttggttcggttcgtgtctatcattatgggaacctcattcttACACC	3790
O	y	435	-----	435
D	b	3791	ctttgtggccagagctgccttgataggagattgttgagaccggcgccgtgtgcttggcag	3850
O	y	435	-----	435
D	b	3851	gtgggaaagactgccttccctgactagtgctggagaccttgccagggcctagagagct	3910
O	y	436	-----SerProleuAlysPheSerProPhegluglPheAr	447
D	b	3911	cttatctgccttggttgccttccctgcgcagccccctcaaatgtctcccttggaggggtttcg	3970
O	y	447	gProSerProSerLeuProgluProthrgluLeuProleuProProleuLeuProPro	467
D	b	3971	gccacgcccccagacctgcgcgagacccacagagagctacttactctcactctctccacccc	4030
O	y	467	oProProSerThrThralProleuProIleargProProSerGlyThrLysLysSerly	487
D	b	4031	gccgcccttcgacaccccccctctcccaatcgtctcccccctcagggagacaaagaaTCCAA	4090
O	y	487	sArgGlyArgGlyArgProIlyArg 495	
D	b	4091	GAGGGGCCGTGGCGTCAAGGCGC 4115	
RESULT 13				
AAH77989				
ID AAH77989 standard; DNA: 843 BP.				
XX AAH77989:				
XX AC				
XX DT 13-NOV-2001 (first entry)				
XX Partial nucleotide sequence of human protein kinase SK216.				
XX				

KM Human; protein kinase; cancer; immune disease; cardiovascular disease;
 KM brain disease; neuronal disease; Alzheimer's disease; chromosome 17;
 KM Parkinson's disease; multiple sclerosis; metabolic disorder;
 KM peripheral nervous system disease; amyotrophic lateral sclerosis;
 KM infection; ocular disease; migraine; pain; sexual dysfunction;
 KM mood disorder; attention disorder; cognition disorder; hypotension;
 KM hypertension; psychotic disorder; dyskinesia; transplant rejection; ss.
 OS Homo sapiens.
 FN WO200166594-A2.
 PD 13-SEP-2001.
 PF 02-MAR-2001; 2001WO-US06838.
 PR 06-MAR-2000; 2000US-0187150.
 PR 29-MAR-2000; 2000US-0193404.
 PR 13-NOV-2000; 2000US-0247013.
 PA (SUGE-) SUGEN INC.
 PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
 DR WPI; 2001-536777/59.
 DR P-PSDB; AAG67390.
 PT Nucleic acids capable of encoding human polypeptides having a kinase or
 PT kinase-like activity, useful for diagnosing a disease selected from
 PT cancers, cardiovascular disease and neuronal-associated diseases (e.g.
 PT Alzheimer's disease) -
 XX
 PS Example 1: Fig 1A; 201pp; English.
 CC The present sequence encodes a partial human protein kinase. The
 CC gene is located at chromosomal position 17q21.2-q22. The kinase
 CC polypeptides are useful for diagnosing a disease or disorder
 CC selected from cancers (e.g. cancers of tissues and cancers of
 CC hematopoietic origin), immune-related diseases and disorders.
 CC cardiovascular disease, brain or neuronal-associated diseases (e.g.
 CC Alzheimer's disease, Parkinson's disease, multiple sclerosis),
 CC metabolic disorders, peripheral nervous system diseases, amyotrophic
 CC lateral sclerosis, viral infections, infections caused by prions,
 CC infections caused by bacteria, infections caused by fungi, ocular
 CC diseases, migraines, pain, sexual dysfunction, mood disorders,
 CC attention disorders, cognition disorders, hypotension, hypertension,
 CC psychotic disorders, dyskinesias, and organ transplant rejection.
 CC Kinase inhibitors are useful for treating diseases and disorders
 CC described above.
 XX
 SQ Sequence 843 BP; 268 A; 173 C; 187 G; 215 T; 0 other;
 Alignment Scores:
 Pred. No.: 1,81e-73 Length: 843
 Score: 1211.50 Matches: 224
 Percent Similarity: 90.07% Conservaive: 30
 Best Local Similarity: 79.43% Mismatches: 27
 Query Match: 46.35% Indels: 1
 DB: 22 Gaps: 1
 US-09-762-258-2 (1-495) x AAH77989 (1-843)
 QY 117 AAlaYsIlleValArgAsnAlaLysAspThrAlaHisThrArgAlaGluArgAsnIleLeu 136
 DB 1 GCAAATGATAGTAAAGAAATCTAAAGATACAGCTCAACAAAGCAAGATGATTTCTG 60
 QY 137 GluSerValIysHisProPheIleValGluLeuAlaTyrAlaPheGlnThrGlyGlyLys 156
 DB 61 GAGGAAGTAAGGCAATCCCTTCATGTGATTTAACTTAAGCTTCCTTCAGACTGTGAAAA 120
 QY 157 LeuTyrLeuIleLeuGluCysLeuSerGlyGlyGluLeuPheThrHisLeuGluArgGlu 176
 DB 121 CTCTACCTCATCTCTGATGATCATGAGGAGGAGAACCTATTATGCAATTAGAAAGAG 180

QY 177 GlyIlePheLeuGluAspThrAlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGly 196
 DB 181 GCAAATTTTATGAAAGACACTCCCTGCTTTTACTTGCGCAAAATCTCCATGGCTTTGGCA 240
 QY 197 HisLeuHisSerGlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSer 216
 DB 241 CATTTACATCAAAAGGGGATCATATACAGACCTGAAACCGGAGAGAAATTCATTCTTAAT 300
 QY 217 SerGlnGlyHisIleLysLeuThrAspPheGlyLeuCysLysGluSerIleHisGluGly 236
 DB 301 CACCAAGGTCATATGAACTAACAGACTTGGACTACGCCAAGAAATCTATTATGATGCA 360
 QY 237 AlaValThrHisThrPheCysGlyThrIleGluTyrMetAlaProGluIleLeuValArg 256
 DB 361 ACAGTCACACACATTTTGTGAAACATAGATATCATGCTGAAATCTTGATGACA 420
 QY 257 SerGlyHisAsnArgAlaValAspTrpTrpSerLeuGlyAlaLeuMetTyrAspMetLeu 276
 DB 421 ACTGGCCACAAATCGTGTGATTTGGTGGAGATTGGGACATTAATGATGACATGCTG 480
 QY 277 ThrGlySerProProPheThrAlaGluAsnArgLysLysThrMetAspLysIleLeuArg 296
 DB 481 ACTGGAGCACCCCAATTTACTGGGGAGAAATGAAAGAAAACATTCACAAATCCTCCAA 540
 QY 297 GlyLysLeuAlaLeuProProTyrLeuThrProAspAlaArgAspLeuValLysLysPhe 316
 DB 541 TGTAACTCAATTTGGCTTCCTTACTACACACAAAGAGCCAGACATCTGTTAAAAGCTG 600
 QY 317 LeuLysArgAsnProSerGlnArgIleGlyGlyProGlyAspAlaAlaAspValGln 336
 DB 601 CTGAAAGAAATAGCTGCTCTCT--CTGGAGCTGGTCTCGGGAGCGCTGAGAAATGCAA 657
 QY 337 ArgHisProPhePheArgHisMetAsnTrpAspAspLeuLeuAlaTrpArgValAspPro 356
 DB 658 GGTCAATCCATTTCTTGAACACATTAACGTGGAAGAACTTCTGCTCAAAAAGGTGGAGCCC 717
 QY 357 ProPheArgProCysLeuGlnSerGluGluAspValSerGlnPheAspThrArgPheThr 376
 DB 718 CCTTTTAAACCTCTGTTCGATCTGAAGAGATGTAAAGTCACTTGATTCCTCAAGTTTACA 777
 QY 377 ArgGlnThrProValAspSerProAspThrAlaLeuSerGluSerAlaAsnGlnAla 396
 DB 778 CGTCAGACACACGTGTGACAGCCACAGATGACCAACTCTCAGTGAACCTCCATATCGAGTGC 837
 QY 397 PheLeu 398
 DB 838 TTTCTG 843
 RESULT 14
 ID ABL16560 standard: DNA; 12396 BP.
 XX
 AC ABL16560;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1153.
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ds.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PF 23-MAR-2001; 2001WO-US09231.
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 18, 2002, 01:29:57 ; Search time 57 seconds
(without alignments)
2663.246 Million cell updates/sec

Title: US-09-762-258-2
2614
Sequence: 1 MARGRRARGAGAAVAEFDL.....PIRPPSGTKSKRGGRGRGR 495

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODL=frame+ p2n model -DEV=xlh
-O=/cgn2_1/USPFO/spool/US09762258/runat_13112002_102445_4910/app_query.fasta_1.647
-DB=issued.patents_NA -OPMT=fastlap -SUFFIX=rml -MINMATCH=0.1 -LOOPCL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=pro -NORM=ext -HEAPSIZE=500 -MITLEN=0 -MAXLEN=200000000
-USER=US09762258.qcgn.1.1.17 @runat_13112002_102445_4910 -NCPU=6 -ICPU=3
-NO_XLPRY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- Issued Patents NA:*
- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
 - 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
 - 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
 - 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
 - 5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq:*
 - 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2594	99.2	1732	4	US-09-430-564-1
2	1947.5	74.5	1637	2	US-08-966-316-10
3	1385.5	53.0	1607	2	US-08-749-902-4
4	806.5	30.9	2370	4	US-09-031-285-1
5	802.5	30.7	2311	4	US-08-712-709-6
6	802.5	30.7	2311	4	US-09-111-444-6
7	802.5	30.7	2311	4	US-09-541-228-6
8	797.5	30.5	1599	3	US-09-256-465-1
9	797.5	30.5	1599	4	US-09-167-332-3
10	796.5	30.5	1276	1	US-07-688-352C-25
11	796.5	30.5	1276	5	PCT-US91-02714-24
12	767.5	29.4	2610	2	US-09-212-771-1

13	767.5	29.4	2610	3	US-09-091-058-1	Sequence 1, Appli
14	752.5	28.8	1273	2	US-08-474-379C-25	Sequence 25, Appl
15	752.5	28.8	1273	3	US-09-146-249A-25	Sequence 25, Appl
16	752.5	28.8	1273	3	US-08-206-188B-25	Sequence 25, Appl
17	719	27.5	2245	4	US-09-225-749-24	Sequence 24, Appl
18	701.5	26.8	2196	4	US-08-313-274-1	Sequence 1, Appli
19	698	26.7	2244	3	US-09-094-714A-48	Sequence 48, Appl
20	669	25.6	2549	4	US-09-467-082-3	Sequence 3, Appli
21	662.5	25.3	2599	6	5266464-1	Patent No. 5266464
22	639.5	24.5	2754	4	US-09-429-332-3	Sequence 3, Appli
23	632.5	24.2	2104	4	US-09-313-930-1	Sequence 1, Appli
24	554	21.2	2160	4	US-09-588-256-1	Sequence 1, Appli
25	551.5	21.1	5720	4	US-09-442-100-1	Sequence 1, Appli
26	547.5	20.9	1935	2	US-08-878-989-11	Sequence 11, Appl
27	547.5	20.9	1935	2	US-09-272-796-11	Sequence 11, Appl
28	540.5	20.7	3018	2	US-08-860-150-6	Sequence 6, Appli
29	540.5	20.7	3018	3	US-09-338-132-6	Sequence 6, Appli
30	540.5	20.7	3984	4	US-09-442-100-3	Sequence 3, Appli
31	537	20.5	3213	4	US-09-442-100-5	Sequence 5, Appli
32	535.5	20.5	2848	4	US-08-464-954A-2	Sequence 2, Appli
33	535	20.5	2101	2	US-08-860-150-1	Sequence 1, Appli
34	535	20.5	2101	2	US-09-338-132-1	Sequence 1, Appli
35	535	20.5	2557	4	US-08-464-954A-1	Sequence 1, Appli
36	532	20.4	1961	4	US-09-509-902A-15	Sequence 15, Appl
37	531.5	20.3	2204	1	US-08-221-817-12	Sequence 12, Appl
38	531.5	20.3	2204	5	US-08-454-439-12	Sequence 12, Appl
39	531.5	20.3	2204	5	PCT-US94-10487-12	Sequence 12, Appl
40	530.5	20.3	1983	1	US-08-221-817-21	Sequence 21, Appl
41	530.5	20.3	1983	1	US-08-454-439-21	Sequence 21, Appl
42	530.5	20.3	1983	5	PCT-US94-10487-21	Sequence 21, Appl
43	521	19.9	3155	4	US-09-442-100-7	Sequence 7, Appli
44	512.5	19.6	688	4	US-08-998-416-90	Sequence 90, Appli
45	508.5	19.5	2206	1	US-08-221-817-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-430-564-1
Sequence 1, Application US/09430564
Patent No. 6372467
GENERAL INFORMATION:
APPLICANT: John Bennis
APPLICANT: Kay K. Lee-Fruman
APPLICANT: Calvin J. Kuo
TITLE OF INVENTION: P54S6K AND P85S6K GENES, PROTEINS,
FILE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
FILE REFERENCE: 00246/506002
CURRENT APPLICATION NUMBER: US/09/430,564
CURRENT FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/106,141
PRIOR FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo sapiens
US-09-430-564-1

Alignment Scores:
Pred. No.: 5,81e-218
Score: 2594.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 99.23%
DB: 4
Gaps: 0

US-09-762-258-2 (1-495) x US-09-430-564-1 (1-1732)
OY 5 Argatgalaatgclglaaglaalaaametalaaalaaalpheaspleuakspuenglutthr 24
|||||
DB 9 CGACGGCCCGCGGGCGCGCGCCGCGCCATGCGCGCGCGTGTGATTGATTGATTTGAGACG 68

[illegible]

QY	385	AspaphrAlaLeuSerGluSerAlaasnGlnAlaPheLeuGluPheThrLyrrValAla	404
Db	1149	GATGACACAGCCCTCCACCGAGAGTCCACMACAGGCTTCTTGCTTCACATACGTGGCG	1208
QY	405	ProSerValLeuaspSerlIelysgluGlyPheSerPheGlnProLysLeuArgSerPro	424
Db	1209	CCGCTGTCCTGGACACATCAAGAGAGGGCTTCTCTTCACCCCAAGCTGGCGTCACCC	1268
QY	425	ArgArgLeuAnaspSerProArgValProValSerProLeuLysPheSerProPheGlu	444
Db	1269	AGGGCCCTCAACATATACCCCGGGTCCCGGTAGGCCCCCTCAAGTTCGCCCTTTGAG	1328
QY	445	GlyPheArgProSerProSerLeuProGluProThrGluLeuProLeuProProLeuLeu	464
Db	1329	GGGTTTGGGCCACCCACACCTGCCGAGCCACACGAGACTACCTTACCTCACTCTCG	1388
QY	465	ProProProProProSerThrThrAlaProLeuProIleArgProProSerGlyThrLys	484
Db	1389	CCACGGCGCGCGCTCGACACAGCGCCCTCTCCCATCCGTCGCCCTCCACGAGACCAAG	1448
QY	485	LysSerLysArgGlyArgGlyArgProGlyArg	495
Db	1449	AAGTCCAGAGAGGGCGCTGGGCGCTCCACAGGGCGC	1481

```

US-08-966-316-10
: Sequence 10, Application US/08966316
: Patent No. 5932445
: GENERAL INFORMATION:
: APPLICANT: Lal, Preeti
: APPLICANT: Au-Young, Janice
: APPLICANT: Reddy, Roopa
: APPLICANT: Murty, Lynn E.
: APPLICANT: Mathur, Preete
: TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/966.316
: FILING DATE: Herewith
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0424 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-855-0555
: TELEFAX: 650-845-4166
: TELEX:
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1637 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: SKINBIT01
: CLONE: 1869688
: US-08-966-316-10

```

Alignment Scores:

Pred. No.:	2.28e-161	Length:	1637
Score:	1947.50	Matches:	407
Percent Similarity:	90.89%	Conservative:	2
Best Local Similarity:	90.44%	Mismatches:	34
Query Match:	74.50%	Indels:	13
		Gaps:	4

US-09-762-258-2 (1-495) x US-08-966-316-10 (1-1637)

```

Qy 9 GlyAlaGlyAlaAlaMetAlaAlaValPheAspLeuAspLeuGluThrGluGlySer 28
Db 180 GGGGGGGGGCCGCCATGGCGCGCGCTGTTGATTGATTGGAGACGAGAGAGGACAC 239
Qy 29 GluGlyGluGlyGluProGluLeuSerProAlaAspAlaCysProLeuAlaGluLeuArg 48
Db 240 GAGGGCGAGGGGCGACCGAGCTCAGCCCCCGGAGCGCATGTCCTCCGCGAGTTGAGG 299
Qy 49 AlaAlaGlyLeuGluProValGlyHisThrGluGluValGluLeuThrGluThrSerVal 68
Db 300 GCAGCTGGCTGACCTGCTGGGACACATGTGAAGAGGTGAGCTGACTGAGACCGAGCTG 359
Qy 69 AsnValGlyProGluArgGlyLeuProHisCysPheGluLeuLeuArgValLeuGlyLys 88
Db 360 AACGTTGGCCGAGCGCATCGGGCCCCCAGCTGCTTGAGCTGCTGGTGCTGGGCAAG 419
Qy 89 GlyGlyThrGlyLysValPheGluValArgLysValGluGlyThrAsnLeuGlyLysIle 108
Db 420 GGGGGCTATGGCAGAGCTTCCAGGTCCAGAAAGGTCCAGACGACCAACTTGGGCAAAATA 479
Qy 109 TyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysAspThrAlaHis 128
Db 480 TATGGCATGAAGTCTTAAGGAAGGCCAAATTTGCGCAATGCCAAGACACAGCACAC 539
Qy 129 ThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPheIleValGluLeuAla 148
Db 540 ACACGGCGTGAAGCGGACATCTAGAGTCAAGAACACCCCTTATTTGGAGACGGCC 599
Qy 149 TyrAlaPheGluThrGlyGlyLysLeuTyrLeuIle-LeuGluCysLeuSerGlyGly 168
Db 600 TATGCGCTTCCAGACGTGGTGGCAACTCACTCACTCTGATTCCTGAGTGGTGGCA 659
Qy 168 uLeuPheThrHisLeuGluArgGlyGlyIlePheLeuGluAspThrAlaCysPheTyrIle 188
Db 660 GCTCTTCACGCACTCTGGAGCGAGAGGCGCATCTTCTGGAAGATACGGCTTCTACT 719
Qy 188 uAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleIleTyrArgAspLe 208
Db 720 GGCTGAGATCAGCGTGGCCCTGGCCATCTCCAGTCCAGGGCATCATCTACGGGACCT 779
Qy 208 uLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeuThrAspPheGlyLe 228
Db 780 CAAGGCCGGAACATCATGCTCAGACGCCAGGCCAACATCAACGCGACTTTGGACT 839
Qy 228 uCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThrIleGluTyr 248
Db 840 CTGCAAGAGGTATTCATCAGAGGCGCGCTCATCACTACCTTCTGGGCAACATGAGTA 899
Qy 248 rMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTyrTyrSerLe 268
Db 900 CATGGCCCTGAGATTCTGTGTCGCGAGTGGCCAAACGGGCTGTGGATGTGGAGGCT 959
Qy 268 uGlyAlaLeuMetTyrAspMetLeuThrGlySerProPhePheThrAlaGluAsnArgLy 288
Db 960 GGGGGCCCTGATGATGAGCATGCTCATCTGATCGCGCCCTTACCGCGAGAACCGGAA 1019
Qy 288 sLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProPheTyrLeuThrProAs 308
Db 1020 GAAAAACATGATGATATCAGGGGCAAGCTGGCACTGCCCTTACTTCACTCAACCCCA 1079
Qy 308 pAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArgIleGlyGlyG 328

```

```

Db 1080 TEGCCGGGACCTTGTCAAAAGTTTCTGAAACGGAATCCACGACGAGTGGGGGTGG 1139
Qy 328 yProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMetAsnTyrAspAs 348
Db 1140 CCCAGGGAGTGTGCTGATGATGACAGACATCCCTTTTCCGACACATGAATTTGGAGCA 1199
Qy 348 pLeuAlaIleTyrValAspProPhePhe-ArgProCysLeuGlnSerGluAspY 368
Db 1200 CTT-CTGGCTTGGCGGTGGANCCCTTTCAGAGGCGCTGTGACGTAGAGAGAGCT 1258
Qy 368 aLserGlnPheAspThrArgPheThrArgGlnThrProValAspSerProAspAspThrA 388
Db 1259 --GACACGATGTATACCCCTTACACAGCGGACAGCGCGGTGACAGTCTGTATGACACAG 1316
Qy 388 lLeuSerGluSerLysAlaGlnAlaPheLeuGlyPheThrTyrValAlaProSerValL 408
Db 1317 C-CTCAGCGAGAGTGGCAACAGCGCTTCTGGGGTT-ACATPAGTGGCGC-TCGTGTC 1373
Qy 408 euAspSerIleLysGluGlyPheSerPheGlnProLysLeuArgSerProArgArgLeuA 428
Db 1374 TGGACAG-ATCAAGAG---TTCCTTTACGCCCAAGT-----GGTCAACGAGGCTC 1423
Qy 428 snSerSerProArgValProValSerProLeuLysPheSerProPheGluGlyPheArgP 448
Db 1424 AANATAGCCCCGGG---TCCGTNAGCCCC---TCAAGTTTNCCTTTNAGGTTGCGCA 1477
Qy 448 roSerProSerLeuProGluProThr 456
Db 1478 GCCACCTTNCNGGCCAAGAGTACT 1503

RESULT 3
US-08-749-902-4
; Sequence 4, Application US/08749902
; Patent No. 5985635
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
; TITLE OF INVENTION: PROTEIN KINASES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,902
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0150 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-845-4166
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:

```

```

CLONE: Consensus
US-08-749-902-4

Alignment Scores:
Pred. No.:      3,76e-112      Length:      1607
Score:          1385.50        Matches:      285
Percent Similarity: 70.65%      Conservative: 40
Best Local Similarity: 61.96%    Mismatches:   69
Query Match:     53.00%         Indels:       67
DB:              2             Gaps:         10

US-09-762-258-2 (1-495) x US-08-749-902-4 (1-1607)

QY      86 LeuGLyLysGLyGLyTyrGLyLysValPheGLnValArgLysValGLnGLyThrAsnLeu 105
      |||||:::|||||:::|||||
Db      227 CTGGGGGAGGGCGCTCATGCGCCGAGTGCAGACCTGC-----ATTAACTGT 271

QY      106 -----GLYSLILETYRAlaMeLysValLeuArg-----LysAla 117
      ::::|:::|:::|:::|:::|
Db      272 ATCACGACGAGGAGTACNCCGTCANANATCATGTGTTTTTNCAGGCCACATTCGGAGC 331

QY      118 LysILEValArgAsnAlaLysAspThrAlaHisThrArgAlaGLuArgAsnILEuGLu 137
      ::::|:::|:::|:::|:::|
Db      332 AGGCTTTCAGGAGGAGTGCAGATGCTTACCAGTCCAGGACACAGAAAGCTCTTAGAG 391

QY      138 SerValLysHisProPheILEValGLuLeuAlaTyrAlaPheGLnThrGLyLysLeu 157
      ::::|:::|:::|:::|:::|
Db      392 CTGATGTAGTTC-----TTGAGGAGGAGGAGCCGCTTC 424

QY      158 TyrILEuILEuGLuLysLeuSerGLyGLyLysLeuPheThrHisLeuGLuArgGLuGLy 177
      |||||:::|:::|:::|:::|
Db      425 TACCTGTGTGTGAGAAAGATGGGGGAGGCTCCATCTGAGCCATCCACAGCCGCGG 484

QY      178 ILePheLeuGLuAspThrAlaCysPheTyrLeuAlaGLuILEThrILEuAlaLeuGLyHis 197
      |||||:::|:::|:::|:::|
Db      485 CACTTCACAGCAGCTGCAGCGCAGCGTGTGTGCAGAGCAGCGGCGACCGCTTGACTTT 544

QY      198 LeuHisSerGLnGLyILEILETYRArgAspLeuLysProGLuAsnILEMetLeuSerSer 217
      |||||:::|:::|:::|:::|
Db      545 CTGCATTAACAAGGAGCATCGCCACAGGAGGACTTAAGCCGGAAACATCTCTGTGACAC 604

QY      218 GLnGLyHis-----ILEYSLILEuThrAspPheGLyLeu----- 228
      ::::|:::|:::|:::|:::|
Db      605 CCCAACCAAGCTTCGCCCGTAGAGATCTGTACTTCGACCTGGCGGCGACCGCATCAATC 664

QY      229 -----CysLysGLuSerILEHisGLuGLyAla-ValThrHisThrPheCysGLyThr 245
      |||||:::|:::|:::|:::|
Db      665 AAGCGGAGCTGCTCCCTAT-CTCCACCGGAGAGCTGCTCACTCG-----TCCGGCTC 717

QY      245 rILEGLuTyrMeLAlaProGLuILE----- 253
      ::::|:::|:::|:::|:::|
Db      718 GCGGAGTACATGCGCCCGGAGTAGTGAGAGGCTTCAGCGAGGAGGCTAGCATCTAGA 777

QY      254 -----LeuValArgSerGLyHisAs 260
      ::::|:::|:::|:::|:::|
Db      778 CAAGCGCTGCGACCTGTGAGACCTGGCGCTCATCTTGTATATCTTACTACTACGCGCTACCC 837

QY      260 nArgAlaValAsp---TrpTrpSer-----LeuGLyAlaLeuMetTyrAspMetLE 276
      |||||:::|:::|:::|:::|
Db      838 GCCCTGTGTGGCGCGCGTGGGAGCGAGCATGCGGCTGGAGCCGTTGATGTAGACATAGCT 897

QY      276 uThrGLySerProPheThrAlaGLuAsnArgLysLysThrMetAspLysILEILEAr 296
      |||||:::|:::|:::|:::|
Db      898 CACTGGATCGCGCGCTTATCCGAGAGAAACCGGAAACCAATGATTAAGATCATCAG 957

QY      296 gGLyLysLeuAlaLeuProPheTyrILEuThrProAspAlaArgAspLeuValLysLysPh 316
      |||||:::|:::|:::|:::|
Db      958 GGGCAAGCTGGACCTTCCCTTACCTACCCCGAGATGCCGGGAGCTTGTCAAAAAAGTT 1017

QY      316 eLeuLysArgAsnProSerGLnArgILEGLyGLyProGLyAspAlaAspValGL 336
      |||||:::|:::|:::|:::|
Db      1018 TCTGAAGGGAATCCACGACGAGATGTGGGGGTGCCCAAGGGAATGCTGTGATGTGCA 1077

```

```

QY      336 nArgHisProPhePheArgHisMetAsnTrpAspAspLeuAlaTrpArgValAspTr 356
      |||||:::|:::|:::|:::|
Db      1078 GAGACATCCCTTTTCCGGACATGATTTGGAGACATTTCTGCGCGGTGTGGACCC 1137

QY      356 oProPheArgProCysLeuGLnSerGLuAspValSerGLIPheAspThrArgPheThr 376
      |||||:::|:::|:::|:::|
Db      1138 CCCTTTAGGCGCTGTCTGACATCAGAGAGAGAGATGAGCAGTTGATATCCCGCTTAC 1197

QY      376 rArgGLnThrProValAspSerProAspThrAlaLeuSerGLuSerAlaAsnGLnAl 396
      |||||:::|:::|:::|:::|
Db      1198 ACGGACAGCCCGGTGACAGTCTGATGACACAGCCCTCAGGAGAGTGCACCAACGAGC 1257

QY      396 aPheLeuGLyPheThrTyrValAlaProSerValLeuAspSerILEYSLuGLyPheSe 416
      |||||:::|:::|:::|:::|
Db      1258 CTCTCTGGCTTACATACATCTGCGCGCTCTGTCTGTGACAGATCAAGAGAGGCTTCTC 1317

QY      416 rPheGLnProLysLeuArgSerProArgArgLeuAsnSerSerProArgValProValSe 436
      |||||:::|:::|:::|:::|
Db      1318 CTTCCAGCCCAAGCTGCGCTCACCCAGGCGCCTTCACAGTAGCCGCCCGGATCCCGTCA 1377

QY      436 rProLeuLysPheSerProPheGLuGLyPheArgProSerProSerLeuProGLuProTh 456
      |||||:::|:::|:::|:::|
Db      1378 CCCCCTCAAGTTCGCCCTTTAGGGGTTTCGCGCCAGCCAGCCTGCGGAGGCCAC 1437

QY      456 rGLuLeuProLeuProProLeuLeuProProProProSerThrThAlaProLeuPr 476
      |||||:::|:::|:::|:::|
Db      1438 GGAGCTACCTTACCTCCTCCTCCAGCCAGCCGCGCCCTTCACACCCCGCTCTCC 1497

QY      476 oILEArgProProSerGLyThrLysLysSerLysArgGLyArgGLyArgProGLyArg 495
      |||||:::|:::|:::|:::|
Db      1498 CATCCGTCGCCCTCAGAGGACCAAGAGTCCAAAGAGGGCGTGGGCTCCAGGCGCT 1555

RESULT 4
US-09-031-295-1
; Sequence 1, Application us/09031295
; Patent No. 6326181
; GENERAL INFORMATION:
; APPLICANT: LANG, Florian
; TITLE OF INVENTION: TAbingen
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLER & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,295
; FILING DATE: 26-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 197-08-173.8
; FILING DATE: 28-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 058315/0123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2370 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

```

; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1335
; US-09-031-295-1

Alignment Scores:
Pred. No.: 3,51e-61 Length: 2370
Score: 806.50 Matches: 172
Percent Similarity: 61.34% Conservative: 66
Best Local Similarity: 44.33% Mismatches: 111
Query Match: 30.85% Indels: 39
Gaps: 12

US-09-762-258-2 (1-495) x US-09-031-295-1 (1-2370)

QY 33 GLUPROGILUeuserProAlaAspAlaCysProLeuAlaGluLeuArgAlaIleuLeu 52
Db 235 GAGCCTGAGCTTATGAAAGCCAAACCTTCTCTCT-----
QY 53 GLUPROVALGlyHIStyrGluGluValGluLeuThrGluThrSerValAsnValGlyPro 72
Db 268 ---CCACCAAGTCTTCTCAGCAA-----ATCAACCTTGCCG 303
QY 73 GLUArgIleGlyProHIScys-----PheGluLeuLeuArgValLeuGlyLys 88
Db 304 TCGTCC---AAATCCATGCTAAACCATCTGACTTTCACCTTCTTGAAGTATGCGGAAG 360
QY 89 GlyGlyTyrglyLysValPheGluValArg---LysValGlnGlyTyHAsnLeuGlyLys 107
Db 361 GGCAGATTGGAAAGGTTCTTCTACAGACACAGCAGCAAGCAAGAAAGTGT-----
QY 108 IleTyHAsnLeuLysValLeuArgPheLysAlaLysIleValArgAsnAlaLysAspThrAla 127
Db 409 TTCTATGAGTCAGCAAGATTTCACAGAAAGCAATCTGAAAAG---AAAGAGAGAG 465
QY 128 HisThrArgAlaGluArgAsnIle---LeuGluSerValLysHisProPheIleValGlu 146
Db 466 CATATTATGTCGAGCGGAAATGTTCTGTGAAGATGTGAAGACACCTTCTGCGTGGGC 525
QY 147 LeuAlaTyHAlaPheGlnThrGlyGlyLysLeuTyHLeuIleLeuGluLysLeuSerGly 166
Db 526 CTTCACCTTCTTCCAAACAGCTGCTGACAAATTTGCTTGTCTGAGTACTATATGAT 585
QY 167 GlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluHisAspThrAlaCysPhe 186
Db 586 GAGAGTTGTTCTTACCATCTCCAGAGAGAGCGCTCTTCTGGAACACAGGCGCTGTTTC 645
QY 187 TyHLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleIleTyHArg 206
Db 646 TATGCTGCTGAATGAGCCAGTGGCTTGGGCTACGTCATCTGCAACATGCTTTATAGA 705
QY 207 AsnLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeuThrAspPhe 226
Db 706 GACTTAAACACAGAAATATTTTCTGATTCACAGGACACATGCTCTTACTGATTTTC 765
QY 227 GlyLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThrIle 246
Db 766 GGACTCTGCAAGAGATTGAACACAAACACACACATCCACTCTGTGGCAGCGG 825
QY 247 GluTyHMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspThrPhe 266
Db 826 GAGTATCTCGCAGCCTGAGTGTTCATTAAGCAGCTTATGACAGAGACGTGAGCTGGTGG 885
QY 267 SerLeuGlyAlaLeuMetTyHAspMetLeuThrGlySerProProPheThrAlaGluAsn 286
Db 886 TGCCGTGGAGCTGCTGTATGATGATGCTGATGGCTGCGCCCTTTTATAGCGGAAC 945
QY 287 ArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProProTyHLeuThr 306
Db 946 ACAAGCTAAATGTACGACACACCTTCTGAAACAGCCTCTCCACCTAAACCAATTTTACA 1005
QY 307 ProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArgIleGly 326

```

```

Db 1006 AATTCGCAAGACACCTCTCTGGAGGGCCTCTCGCAGAGACAGACAAAGCGGCTC--- 1062
QY 327 GlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMetAspThr 346
Db 1063 GGGGCCAAGATGATTCATGAGATGAGATTAAGAGTCACTGATCTTCTTAAATTAACGTG 1122
QY 347 AspAspLeuLeuAlaTyHArgValAspProProPheArgProCysLeuGluSerGluGlu 366
Db 1123 GATGATCTCATTAATAAGAGTTTACTCCCTTTTAAACCCAAATGTAGTGGGCCAAC 1182
QY 367 AspValSerGlnPheAspThrArgPheThrArgGlnThrProVal----- 381
Db 1183 GAGTACAGGACCTTGACCCCGAGTTTACCGAAGAG---CTGTCCCAACTCATTCATGCG 1239
QY 382 AspSerProAspAsp-----ThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeu 398
Db 1240 AAGTCCCTGACAGCGTCTCTGACAGCCAGCGTCAAGGAGAGTGGCAGGCTTTCCTA 1299
QY 399 GlyPheThrTyHValAlaProSer 406
Db 1300 GGCCTTCTCTATGCGGCTCCACG 1323

RESULT 5
US-08-712-709-6
; Sequence 6, Application US/08712709
; Patent No. 5863780
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/712,709
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-845-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2311 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
; US-08-712-709-6

Alignment Scores:
Pred. No.: 7.57e-61 Length: 2311
Score: 802.50 Matches: 172
Percent Similarity: 61.08% Conservative: 65
Best Local Similarity: 44.33% Mismatches: 112
Query Match: 30.70% Indels: 39

```

```

DB: 2 Gaps: 12
US-09-762-258-2 (1-495) x US-08-712-709-6 (1-2311)
QY 33 GlnProGluLeuSerProAlaAspAlaCysProLeuAlaGluLeuArgAlaAlaGlyLeu 52
DB 202 GAGCCTGAGCTTATGATGATGCAACCCCTTCCTC----- 234
QY 53 GlnProValGlyHisTyrGluGluValGluLeuThrGluThrSerValAsnValGlyPro 72
DB 235 ---CCACCAGTCTCTTCAGCAA-----ATCAACCTTGCGCCG 270
QY 73 GlnArgGlyLeuGlyProHisCys-----PheGluLeuLeuArgValLeuGlyLys 88
DB 271 TCGTTC---AATGCTCATGCTAAACCATCTGACTTCCTTCATTCGAAAGATCGGAAG 327
QY 89 GlyGlyTyrGlyValLeuPheGlnValArg---LysValGlnGlyThrAsnLeuGlyLys 107
DB 328 GGCAGTTTGGAAAGGTTCTCTAGCAAGACACAGCAAGCAAGAGAGT----- 375
QY 108 IleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysAspThrAla 127
DB 376 TTCTATGCACTCAAGTTTACAGAGAAAGCAATCTGAAAAAG---AAGAGAGAGAG 432
QY 128 HisThrArgAlaGluArgAsnIle---LeuGluSerValLysHisProPheIleValGlu 146
DB 433 CATATTATGTCGGAGCGGATGTTCTGTGAGAAATGTGAAGCACCCTTCCTGTCGGGC 492
QY 147 LeuAlaTyrAlaPheGlnThrGlyLysLeuTyrIleLeuGluCysLeuSerGly 166
DB 493 CTTCACCTTCCTTCCTGAGCTGTCGACAAATGTACTTCTCCTAGACTACATTAAATGT 552
QY 167 GlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCysPhe 186
DB 553 GAGAGAGTTGTTCAACCTCTCCAGAGGAAAGCGCTTCCTGACACAGCGGCTTC 612
QY 187 TyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleIleTyrArg 206
DB 613 TATGCTGCTGAATATGACCACTGCTGGCTACCTGCATCAGACATCGTTATAGA 672
QY 207 AspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeuThrAspPhe 226
DB 673 GACTTAAACAGAGATATTTGCTAGATTTCACAGGGAACCATTCCTTACAGACTTC 732
QY 227 GlyLeuCysLysGluSerIleHisGluGlyAlaValAlaThrHisThrPheCysGlyThrIle 246
DB 733 GGACTCGCAAGAGGAAATGAAACACACAGCAACATCCACTCTGTGGCAGCCG 792
QY 247 GluTyrMetLarProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTyrTrp 266
DB 793 GAGTATCTCCACCTGAGGTGCTTCATATAGCAGCTTATACAGAGACTGTGAGCTGTGG 852
QY 267 SerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThrAlaGluAsn 286
DB 853 TGCCTGGAGACTGCTGTGTATGATGCTGTATGAGCTGCGCGCTTTTATAGCCGAAC 912
QY 287 ArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProTyrLeuThr 306
DB 913 ACAGCTGAATGTAGCAACATTCGACACAGCCTCTCCAGCTGAACCAATATATACA 972
QY 307 ProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArgIleGly 326
DB 973 AATTCCGCAACACCTCTCGAGGCGCTCTCGACAGAGACAGCAAGCGGCTC--- 1029
QY 327 GlyGlyLysProGlyAspAlaAlaAspValGlnArgHisProPheArgHisMetAspTrp 346
DB 1030 GGGGCCCAAGATGACTTCATGAGATTAAAGATCATGTCTTCTTCCTTAATTAATCGG 1089
QY 347 AspAspLeuLeuAlaTyrArgValAspProProPheArgProCysLeuGlnSerGluGlu 366
DB 1090 GATGATCTCTATTAATAAGAAATTAATCCCTTTTAACCAATATGAGTGGGCCCAAC 1149
QY 367 AspValSerGlnPheAspThrArgPheThrArgGlnThrProVal----- 381

```

```

DB 1150 GACCTACGGCAGCTTACCGCGAGGTTTACCGAAGAG---CCTGCCCCCACTCATTTGCC 1206
QY 382 AspSerProAspAsp-----ThrAlaLeuSerLysIleAsnGlnAlaPheLeu 398
DB 1207 AAGTCCCTGAGCAGCGCTCGTCACAGCCAGCGTCAAGAAAGCTGCCGAGGCTTCTTA 1266
QY 399 GlyPheThrTyrValAlaProSer 406
DB 1267 GGCCTTCTATGCGCTCCACAGC 1290

RESULT 6
US-09-111-444-6
; Sequence 6, Application US/09111444
; Patent No. 6045792
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,444
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ. ID NO.: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2311 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
; US-09-111-444-6

Alignment Scores:
Pred. No.: 7,57e-61 Length: 2311
Score: 802.50 Matches: 172
Percent Similarity: 61.08% Conservative: 65
Best Local Similarity: 44.33% Mismatches: 112
Query Match: 30.70% Indels: 39
DB: 3 Gaps: 12

US-09-762-258-2 (1-495) x US-09-111-444-6 (1-2311)
QY 33 GlnProGluLeuSerProAlaAspAlaCysProLeuAlaGluLeuArgAlaAlaGlyLeu 52
DB 202 GAGCCTGAGCTTATGATGATGCAACCCCTTCCTC----- 234
QY 53 GlnProValGlyHisTyrGluGluValGluLeuThrGluThrSerValAsnValGlyPro 72

```



```

Db 235 ---CCACCAAGTCCTCTCAGCAA-----ATCAACCTTGCGCCG 270
QY 73 GUAArgIleGlyProHisCys-----PheGluLeuLeuArgValLeuGlyLys 88
Db 271 TCGTCC---AATCTCATGCTTAACCAATCTGACATTCCTTCTGAAGATCGGAAG 327
QY 89 GUGlyTyrgIlyLysValPheGlnValArg---LysValGlnGlyThrAsnLeuGlyLys 107
Db 328 GGCAGTTTGGAAAGGTTCTTCTAGCAAGACAAAGGAGAGAAAGT----- 375
QY 108 IleTyraIleMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysAspThrAla 127
Db 376 TTCTATGAGATCAAGATTTTACAGAAAGCAATCTCGAAAG---AAGAGAGAGAG 432
QY 128 HisThrArgAlaGluArgAsnIle---LeuGluSerValLysHisProPheIleValGlu 146
Db 433 CATATTATGTCGGAGCGGAATGTTCTGTGAAGATGTGAAGCAACCTTCTGCTGGCGC 492
QY 147 LeuAlaTyraIlePheGlnThrGlyLysLeuTyraIleGluLeuGluCysLeuSerGly 166
Db 493 CTTACATCTTCTTCCAGACTGCTGACAAATTTGACTTGTCTTACACTACATTATGCT 552
QY 167 GUGlyLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCysPhe 186
Db 553 GGAGAGTTGTTCTACACATCTCCAGAGGAGACGCTGCTTCTGGAACACGGGCTGCTCC 612
QY 187 TyraLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleIleTyraArg 206
Db 613 TATCTCTGCTGAATAAGCCAGTGGCTTGGCTGACCTGACATCTGACATGATGTTATAGA 672
QY 207 AspleuLysProGluAsnIleMetLeuSerGlnGlyHisIleLysLeuThrAspPhe 226
Db 673 GACTTAACACGAGAAATATTTGCTAGATTACAGGAGACATGCTTCTTACCTGACTGC 732
QY 227 GUGlyCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThrIle 246
Db 733 GGACTGTCGACGAGAGAACATTGAAACACAAACAGACATCACCCTTGTGGCAGCGCG 792
QY 247 GUGlyThrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspThrTrp 266
Db 793 GAGTATCTCCGACCTGAGGCTCTTCATTAAGCAGCCTTATGACAGACCTGAGCGTGG 852
QY 267 SerLeuGlyAlaLeuMetLysAspMetLeuThrGlySerProProPheThrAlaGluAsn 286
Db 853 TGCCTGGAGGCTGCTTATGAGATGCTATAGGCTGACCGCCTTTTATAGCCGAAC 912
QY 287 ArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProTyraIleThr 306
Db 913 ACAGCTGAATGTTAGACAAACATTTCTGAACAAGCCTTCCAGCTGAACCAATATTACA 972
QY 307 ProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArgIleGly 326
Db 973 AATTCGCCAAGACACCTTCCGAGGCGCTCTGCGAAGAGCAGACGAAACAGCGCTC--- 1029
QY 327 GUGlyLysProGluAspAlaIleAspValGlnArgHisProPheArgHisMetAspThr 346
Db 1030 GGGGCCAAGATGATTCATGAGATTAAGAGTCACTGCTTCTTCTTATTAATACGTGG 1089
QY 347 AspAspLeuLeuAlaTrpArgValAspProPheArgProCysLeuGlnSerGluLys 366
Db 1090 GATGATTCATTAATAAGAAATTAATACCTCCCTTTTAACCAAAAGTGAAGGCGCCAAC 1149
QY 367 AspValSerGlnPheAspThrArgPheThrArgGlnThrProVal----- 381
Db 1150 GACCTTACGCACTTTGACCCGAGTTTACCGAAGAG---CCTGTGCCCACTCCATTGGC 1206
QY 382 AspSerProAspAsp-----ThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeu 398
Db 1207 AAGTCCCTTGACAGCGTCTCTGTACAGCCAGCGTCAAGAGAGCTGCCGAGGCTTCTCA 1266
QY 399 GlyPheThrTyraIleAlaProSer 406
|||||
|||||

```

```

Db 1267 GCGTTTCTTCTATGCGCTCCACAG 1290
RESULT 7
US-09-541-228-6
; Sequence 6, Application US/09541228
; Patent No. 6232077
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/541,228
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PR-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2311 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-09-541-228-6
Alignment Scores:
Pred. No.: 7.57e-61 Length: 2311
Score: 802.50 Matches: 172
Percent Similarity: 61.08% Conservative: 65
Best Local Similarity: 44.33% Mismatches: 112
Query Match: 30.70% Indels: 39
DB: 4 Gaps: 12
US-09-762-258-2 (1-495) x US-09-541-228-6 (1-2311)
QY 33 GUGProGluLeuSerProAlaAspAlaCysProLeuAlaGluLeuArgAlaIleGlyLeu 52
Db 202 GAGCTGAGCTTATGAATGAAGCCAAACCTTCTCTCT----- 234
QY 53 GUGProValGlyHisTyrgIleGluGluValGluLeuThrGluThrSerValAsnValGlyPro 72
Db 235 ---CCACCAAGTCCTTCTCAGCAA-----ATCAACCTTGCGCCG 270
QY 73 GUAArgIleGlyProHisCys-----PheGluLeuLeuArgValLeuGlyLys 88
Db 271 TCGTCC---AATCTCATGCTTAACCAATCTGACATTCCTTCTGAAGATCGGAAG 327
QY 89 GUGlyTyrgIlyLysValPheGlnValArg---LysValGlnGlyThrAsnLeuGlyLys 107
|||||
|||||

```

Db 328 GGCAGTTTGGAAAGCTTCTTAGCAGACACAGGCGACAGAGT----- 375
 Qy 108 lletyAlametyValleuArgylsAlaLyslleValArgsnalLysAspThrAla 127
 Db 376 TTTATGACGTCAAGTTTACAGAGAAAGCAATCTGAAAAG---AAGAGGAGAAC 432
 Qy 128 HistHrArgAlaLysArgsnlle---LeuGluSerValLysHisProPheIleValGlu 146
 Db 433 CATATTATGTCGAGCGAAGATTTCTGTGTGAAAGATGTGAAAGACCTTCTGTCGGCC 492
 Qy 147 lletyAlaLysPheGlnThrGlyLysLeuThrLeuLysGluCysLeuSerGly 166
 Db 493 CTTCACCTCTCTTCCAGAGCTGTGACAAATTTACTTTCTTAGACATCAATTAAAGT 552
 Qy 167 GlyLysLeuPheThrHisLeuGluArgGlyLysIlePheLeuGluAspThrAlaCysPhe 186
 Db 553 GAGAGAGTTGTTTACCATCTCCAGAGGAGAGCGTGTCTCTGAGAACCGGGCTCGTCC 612
 Qy 187 TyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleIleTyrArg 206
 Db 613 TATGCTGCTGAAATAGCCAGCTGCTGGCTTACCTGCATTCACATGAACTGTTATAGA 672
 Qy 207 AspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeuThrAspPhe 226
 Db 673 GACTTAAACACAGAAATATTTGCTAGATTCAAGGACACATGTCTCTTACTGACTTC 732
 Qy 227 GlyLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThrIle 246
 Db 733 GGACTCTGCAGAGAGCAATTTGAAACACAGCAACAAACATCCACTCTGTGGACGCCG 792
 Qy 247 GluTyrMetLysProGluIleLeuValArgSerGlyHisAsnArgAlaValAspThrPhe 266
 Db 793 GACTATCTCCACCTGAGGCTTCATAGCACCTTATACAGAGCTGTGGCTGTGG 852
 Qy 267 SerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProPheThrAlaGluAsn 286
 Db 853 TGCTTGAGACTCTCTTGTATGAGATGCTTATAGCCCTGCCCTTTTATAGCCGAAC 912
 Qy 287 ArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProPheTyrLeuThr 306
 Db 913 ACAGCTGAATGTACGACAACTTTCGAAACAGCTCTCAGTGAACCAATATATACA 972
 Qy 307 ProAspAlaLysArgsnlleValLysLysPheLeuLysArgsnProSerGlnAlaGlyIle 326
 Db 973 AATTCGCGAAGACACTCTCGAGGGCTCTGACAGAGACAGCAAGACGCGCTC--- 1029
 Qy 327 GlyLysProGluAsnAlaAspValGlnArgHisProPheArgHisMetAsnThr 346
 Db 1030 GGGGCCAAGATGACTTCATGAGAGATTAGAGTATGCTTCTTCTTAATTAACTGG 1089
 Qy 347 AspAspLeuLeuAlaTrpArgValAspProPheArgProCysLeuGlnSerGluGln 366
 Db 1090 GATGATCTCATTTATAGAAAGATTACTCCCTTTTAAACCAATGTAGTGGGCCAAC 1149
 Qy 367 AspValSerLysIleAspThrArgPheThrArgGlnThrProVal----- 381
 Db 1150 GACCTACGGGACCTTGAACCCGAGTTTACCGAAGAG---CCTGTCCCAATCCATTGGC 1206
 Qy 382 AspSerProAspAsp-----ThrAlaLeuSerGlnSerLysAsnGlnAlaPheLeu 398
 Db 1207 AAGTCCCTACAGCGCTCTGTCACAGCCAGCTCAAGAGACTGCCGAGGCTTCTCTA 1266
 Qy 399 GlyPheThrTyrValAlaProSer 406
 Db 1267 GGCTTTTCTATGCGCTCCACG 1290

; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
 ; FILE REFERENCE: RTS-0035
 ; CURRENT APPLICATION NUMBER: US/09/256,465
 ; CURRENT FILING DATE: 1999-02-23
 ; NUMBER OF SEQ ID NOS: 47
 ; SEQ ID NO 1
 ; LENGTH: 1599
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (88)..(1533)
 US-09-256-465-1
 Alignment Scores:
 Pred. No.: 1,2e-60 Length: 1599
 Score: 797.50 Matches: 168
 Percent Similarity: 59.858 Conservative: 69
 Best Local Similarity: 42.428 Mismatches: 130
 Query Match: 30.514 Indels: 29
 Gaps: 8
 US-09-762-258-2 (1-495) x US-09-256-465-1 (1-1599)
 Qy 48 ArgAlaAlaGlyLeuGluProValGlyHis-----TyrGluGlu 60
 Db 424 CGGGCCCGAGCGAGACCCCATGAGTACAGTGTGCTCCCGCAGTACCTCCACG 483
 Qy 61 ValGluLeuThrGluThrSerValAsnValGlyProGluArgIleGlyProHisCysPhe 80
 Db 484 ACTGAGAGATGAGTGGGGGTGACAGAGCGAGGAGCTTAACTGAATGACTTC 543
 Qy 81 GluLeuLeuArgValLeuGlyLysGlyLysValPheGlnValArgLysVal 100
 Db 544 GACTATCTCAAACTCTCTGCGAAGAGCTTGGCAAGTCACTCGTGTGGGAG--- 600
 Qy 101 GlnGlyThrAsnLeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleVal 120
 Db 601 -----AAGCCACCTGGCCCTACTAGCCCATGAAGTCTCGGAAAGCAATCATATT 654
 Qy 121 ArgAsnAlaLysAsp---ThrAlaHisThrArgAlaGluArgsnIleLeuGluSerVal 139
 Db 655 -----GCCAAGATGAAGTGGCTCACACAGTACAGGAGCGGGCTCTCCGAACAC 708
 Qy 140 LysHisProPheIleValGluLeuAlaTyrAlaPheGlnThrGlyLysLeuTyrLeu 159
 Db 709 AGGCACCCGTTCTCACTGCTGAGTATGCTTCACAGCCACGACGCGCTGCTTT 768
 Qy 160 IleLeuGluCysLeuSerGlyGlyGluLeuPheThrHisLeuLysArgGluGlyIlePhe 179
 Db 769 GTGATGAGATGATCCCAACGGGGGTGAGCTGTCTTCACCTGTCCCGGAGCGTGTTC 828
 Qy 180 LeuGluAspThrAlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlnHisLeuHis 199
 Db 829 ACAGAGAGAGCGGGCCGGTTTATGTCGACAGATTTGTCTGCTTGAATCTTGGAC 888
 Qy 200 SerGlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGly 219
 Db 889 TCGCGGAGACTGTATACCGGACATCAAGCTGGAAGAACTCATGCTGGAGCAAGATGGC 948
 Qy 220 HisIleLysLeuThrAspPheGlyLeuCysLysGluSerIleHisGluGlyAlaValThr 239
 Db 949 CACATCAAGATCACTGCTTGTGGCTGTGCAAGAGGCGCATGAGTACGGGCGCACCATG 1008
 Qy 240 HisThrPheCysGlyThrIleGlyTyrMetAlaProGluIleLeuValArgSerGlyHis 259
 Db 1009 AAAACCTTGTGTGGAGCCCGGAGTACTGCGCTGAGGTGAGAGCAATGACTAT 1068
 Qy 260 AsnArgAlaValAspTrpPheSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySer 279
 Db 1069 GGGCGGGCCGTGACGTGTGGGGCTGTGGTGTATGACAGATGATGTGGGCCCGC 1128
 Qy 280 ProPheThrAlaGluAsnArgLysLysThrMetAspLysIleIleArgGlyLysLeu 299

RESULT 8
 US-09-256-465-1
 ; Sequence 1, Application US/09256465
 ; Patent No. 6043090
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Lex M. Cowsett

Db 1129 CTGCCCTTCTACACACGACGACGAGCGCTCTTCGAGCTCATCTCATGGAAGACATC 1188
QY 300 AAlaLeuProProTyrLeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArg 319
Db 1189 CGCTTCGCCGCGACCTGACCGCCGAGGCGCAAGTCCCTGCTGAGCGCTGCTTAAGAAG 1248
QY 320 AsnProSerGlnArgIleGlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisPro 339
Db 1249 GACCCCAAGCAGAGGCTTGTTGGTGGGGGCCACCGATGCCAAGAGGTATGAGACACAGG 1308
QY 340 PhePheArgHisMetAsnTyrAspAspLeuLeuAlaTyrArgValAspProPheArg 359
Db 1309 TTCTCTCCAGCATCACTACGCGAGACGCTGTCAGAGAAGACCTCTGACACCTTCAAA 1368
QY 360 ProCysLeuGlnSerGlyGlyAspValSerGlnPheAspThrArgPheThrArgLys 378
Db 1369 CCTCAGCTCAGCTCCGAGGTGCACAAAGTACTTCGATGAAATTAACCCCGCAGTCC 1428
QY 379 -----ThrProValAspSerProAspAspThrAlaLeuSerGlySerAlaAsnGln 395
Db 1429 ATCAACATCAACACCCCTGACCGCTATGACAGCTGGCTTACTGAGCTGACACAGCG 1488
QY 386 Ala-----PheLeuGlyPheThrTyr-----ValAlaPro--- 405
Db 1489 ACCCACTTCCCGCCAGTTCCTCTACACGCGCAGCATCCGCGAGTGAAGACGTGCCACGC 1548
QY 406 -----SerValLeuAspSerIleLysGlyGlyPheSerPheGlnPro 419
Db 1549 AGAGAGCCAGCGCTCGTCCATCACCGCTGGGTGTTTATACCCCT 1596

RESULT 9

US-09-167-322-3
Sequence 3, Application US/09167322
Patent No. 6365151

GENERAL INFORMATION:

APPLICANT: Allegheny University of the Health
Sciences, Halpern, Michael S.
England, James M.

TITLE OF INVENTION: CANCER VACCINE
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESS: Seidel, Gonda, Lavorigna & Monaco, P.C.
STREET: Suite 1800, Two Penn Center Plaza
CITY: Philadelphia

STATE: PA
COUNTRY: USA

ZIP: 19102

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/167,322
FILING DATE: 07-Oct-1998

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/00582

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 7933-33 PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 1599 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-167-322-3

Alignment Scores:
Pred. No.: 1.2e-60 Length: 1599
Score: 797.50 Matches: 168
Percent Similarity: 59.85% Conservative: 69
Best Local Similarity: 42.42% Mismatches: 130
Query Match: 30.51% Indels: 29
DB: 4 Gaps: 8

US-09-762-258-2 (1-495) x US-09-167-322-3 (1-1599)

QY 48 AAlaAlaGlyLeuGluProValGlyHis-----TyrGluGlu 60
Db 424 CGGCGCCCGCAGGAGGAGGACCCCTGACACTCAAGTGTGCTCCCGCAGTACCTCCACG 483
QY 61 ValGluLeuThrGluThrSerValAsnValGlyProGluArgIleGlyProHisCysPhe 80
Db 484 ACTGAGGAGATGGAAGTGGCGGTGACAGCAGGCGCTAAAGTGCATGAAATGACTTC 543
QY 81 GluLeuLeuArgValLeuGlyLysGlyGlyTyrGlyLysValPheGlnValArgLysVal 100
Db 544 GACTATCTCAAACTCTTGGAAGGAACTTTGGCAAGTCACTCTGTCGGGAG--- 600
QY 101 GlnGlyThrAsnLeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleVal 120
Db 601 -----MAGCCACTGCGCGCTACTACGCTCAAGATCTCTCGAAGAAGTCACTATT 654
QY 121 ArgAsnAlaLysAsp---ThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerVal 139
Db 655 -----GCCAAGAGTGAAGTCCCTCACACAGTACACGAGCGGGTCTCCAGAAACACC 708
QY 140 LysHisProPheIleValGluLeuAlaTyrAlaPheGlnThrGlyLysLeuThrLeu 159
Db 709 AGGACACCCCTCTCTCACTGCTGAAGTATGCTTCCACACGACCGCCTGCTTT 768
QY 160 IleLeuGlyCysLeuSerIleGlyGlyLeuPheThrHisLeuGluArgLysIlePhe 179
Db 769 GTGATGAGATATGCCACGAGGGGTGAGCTGTTCTTCCACTCTCCGCGAGCGTGTCTTC 828
QY 180 LeuGluAspThrAlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHis 199
Db 829 ACAGAGACGCGGCGCGGTTTATGGTGACAGATGTCTCGGCTGTGATCTTGAC 888
QY 200 SerGlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGly 219
Db 889 TCGCGGAGCTGTATACCGCACATCAAGCTGAAACCCTCATGCTGGAACAAAGATGGC 948
QY 220 HisIleLysLeuThrAspPheGlyLeuCysLysGluSerIleHisGluGlyAlaValThr 239
Db 949 CACATCAAGATCACTACTTGTGGCTCTGCAAAAGAGGATCAGTACGCGGCGCACCATG 1008
QY 240 HisThrPheCysGlyThrIleGlyLysMetAlaProGluIleLeuValArgSerGlyHis 259
Db 1009 AAACCTTCTGAGGACCCCGGAGTACCTGCGCGCTGAGAGGTGCTGAGGACATGACTAT 1068
QY 260 AsnArgAlaValAspTyrPhePheSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySer 279
Db 1069 GCGCGGCGCGTGAAGTGGGGGGGTGGGTGCTATAGCAAGTATGATGTCGGCGCCG 1128
QY 280 ProPheThrAlaGluAsnArgLysLysThrMetAspLysIleIleArgLysLysLeu 299
Db 1129 CTGCCCTTACACACGACGACGAGCGCTTGTGAGCTCATCTCATGGAAGAGATC 1188
QY 300 AAlaLeuProProTyrLeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArg 319
Db 1189 CGCTTCGCCGCGACGCTCAGCCCGGAGGCAAGTCTCTGCTGCGCTTAAGAAG 1248
QY 320 AsnProSerGlnArgIleGlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisPro 339
Db 1249 GACCCCAAGCAGAGGCTTGTTGGTGGGGGCCACGAGTGCCAAGAGGTATGAGACACAGG 1308

QY 340 PhephearHtHmetantTPaspAspLeuLeuAlaTPPrArgValaAspProPheArg 359
 Db 1309 TTCTTCTTCAGCATCACTGGCAGGAGCTGCTCCAGAGAGCTCCGACCCCTTCAA 1368
 QY 360 ProcysLeuGlnSerGluGluAspValSerGlnPheAspThrArgPheThrArgGln--- 378
 Db 1369 CCTCAGGTCCAGTCGCGAGGTCGACACAGAGTACTTCATATGATGATTACGCCCTCC 1428
 QY 379 -----ThrProValaAspSerProAspPThrAlaLeuSerGlnAsnGln 395
 Db 1429 ATCAATCATACACCCCTGACCGCTATGACAGCGCTTACTGAGCTGAGACCAAGCG 1488
 QY 396 Ala---PheLeuGlyPheThrTyr-----ValaAlaPro--- 405
 Db 1489 ACCCACTTCCCGCATCTCTCTACTCGCGACGATCCGCGAGAGCATCTGCCACGC 1548
 QY 406 -----SerValaLeuAspSerIleGluGlyPheSerPheGlnPro 419
 Db 1549 AGAGGACGACGCTCGCTGCTATCACCCTGCGGTGGTTTTCACCCCT 1596
 RESULT 10
 US-07-688-352C-25
 ; Sequence 25, Application us/07688352C
 ; Patent No. 5527896
 ; GENERAL INFORMATION:
 ; APPLICANT: Wigler, Michael H.
 ; APPLICANT: Colicelli, John J.
 ; TITLE OF INVENTION: Cloning by Complementation and Related
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; ADDRESS: Bicknell
 ; STREET: Two First National Plaza, 20 South Clark
 ; CITY: Street
 ; STATE: Chicago
 ; COUNTRY: USA
 ; ZIP: 60603
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/688,352C
 ; FILING DATE: 19910419
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/511,715
 ; FILING DATE: 20-APR-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Borun, Michael F.
 ; REGISTRATION NUMBER: 25447
 ; REFERENCE/DOCKET NUMBER: 27805/30197
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 346-9750
 ; TELEFAX: (312) 984-9740
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ. ID NO: 25:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1276 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 2..504
 ; US-07-688-352C-25
 Alignment Scores: 1.05e-60 Length: 1276
 Pred. No.:

Score: 796.50 Matches: 182
 Percent Similarity: 64.14% Conservative: 63
 Best Local Similarity: 47.64% Mismatches: 110
 Query Match: 30.47% Indels: 32
 DB: 1 Gaps: 4
 US-09-762-258-2 (1-495) x US-07-688-352C-25 (1-1276)
 QY 29 GluGlyGluGlyGluProGluLeuSerProAlaAspAlaCysProLeuAlaGluLeuArg 48
 Db 71 GAACCTATGGGAGAGGAGGAGATTAACCA----- 100
 QY 49 AlaAlaGlyLeuGluProValaGlyHisTyrGluGluValGluLeuThrGlnSer--- 67
 Db 101 -----CAACCTGAAGATCGTATCAAGAAATTCGAAATC 136
 QY 68 -----ValaAsnValGlyProGluArgIleGlyProHisCysPheGluLeuArg 84
 Db 137 ACACATCATGTAAAGAGAGACATGAAGAGCGAGATCTCCAGTTGACACTTTTAA 196
 QY 85 ValLeuGlyLysGlyGlyTyrGlyLysValPheGlnValArgLysValGlnGlyThrAsn 104
 Db 197 GTATTAGGCGAGGATCATTTGGAAAGCTTTCTTGTTAAATAATCTCAGGCTCGAT 286
 QY 105 LeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLys 124
 Db 257 GCTAGGACGCTTTATGATCATGAAGATTAAGAGAGCCACACTG-----AAAGTTCGA 310
 QY 125 AspThrAlaHisThrArgAlaGluArgAsnIleLeuGlnSerValLysHisProPheIle 144
 Db 311 GACCGAGCTTGGACAAATAAGACGATGATCTTGTGAGGTTATCATCTTTATT 370
 QY 145 ValGluLeuValTyrAlaPheGlnThrGlyGlyLysLeuTyrTyrLeuLeuGluCysLeu 164
 Db 371 GTCAAGTTCATATATCT-TTCAAACTGAAGGAGAGTGTATCTTAT-TTGATTTTCTC 428
 QY 165 SerGlyGlyLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAla 184
 Db 429 AGGGAGAGATTTGTATCACGCTTATCCAAAGAGGTATGATCCAGAAAGATGTC 488
 QY 185 CysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIle 204
 Db 489 AAATTCTACCTGGCTGACACTTCGACTTGTAGACCCTTACNTACCTGGGAATAATT 548
 QY 205 TyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlnHisIleLysLeuThr 224
 Db 549 TATAGAGACTTAACACAGAAATATCTT-CTTGAGGAAGAGAGTCACATCAAGTTAA 607
 QY 225 AspPheGlyLeuCysLysGlnSerIleHisGluGlyAlaValThrHisThrPheCysGly 244
 Db 608 GATTTGGCGCTAAGTAAGAGTCTATTGACCATGAAGAAAGCAATATCT-TTTTGTGGA 666
 QY 245 ThrIleGluTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValaAsp 264
 Db 667 ACTGTGAGATATAGGCTCCAGAAAGTAATGATGTCGAGAGTATATCTCGAAGTCTGAC 726
 QY 265 TyrTrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerPro-ProPheThrAl 284
 Db 727 TGGTGGCTTTTGGTGGTTAAAGTTGAATCTTAAGTGTGACATCCCTTCCAAAG 786
 QY 284 GluAsnArgLysLysThrMetAspLysIleIleArgGly-LysLeuAlaLeuProProt 304
 Db 787 AAAGATCGAAGAAAGAAACATGACTATGATCTTAAAGCCAAACCTGGAAATCCACAG 846
 QY 304 TyrLeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGln 324
 Db 847 TTTGAGTCTCGAAGCGCAGAGCTTTACGAATGCTTTTAAAGCGAAATCTGCAAGC 906
 QY 324 rglIleGlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHis 344
 Db 907 GATTAGGTGACGACGACGAGATGAGGTTGAAGAATTTAAAGACATCTATTTTCTCAAG 966
 QY 344 etasntTPaspAspLeuLeuAlaTPPrArgValaAspProPheArgProCysLeuGln 364

Db 967 TAGACTGAATAACTGATAGAGA-GAATTCATCCGCCATTTAAACCTCAACGGCA 1025
QY 364 ergluGluaspValserGlnPheaspThrArgPheThrArgGlnThrProValaspSerp 384
Db 1026 GGCCGTGAATACATCTTATTTTGTATCTGAGTTACTGCAAAAACCTCCAAATTCAC 1085
QY 384 roaPaapThrAlaLeuSerGluSerAlaasnGlnAlaPheLeuGlyPheThrTyVala 404
Db 1086 CT---GGCATTCACCTAGTCTCTAATGCACATCAGCTTTTCGGGGGTTTGTGTTG 1142
QY 404 la 404
Db 1143 CT 1144
RESULT 11
PCT-US91-02714-24
Sequence 24, Application PC/TUS9102714
GENERAL INFORMATION:
APPLICANT: Migler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02714
FILING DATE: 19910419
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 27805/30197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1276 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2..504
PCT-US91-02714-24
Alignment Scores:
Pred. No.: 1.05e-60 Length: 1276
Score: 796.50 Matches: 182
Percent Similarity: 64.14% Conservative: 63
Best Local Similarity: 47.64% Mismatches: 110
Query Match: 30.47% Indels: 32
Gaps: 4

us-09-762-258-2 (1-495) x PCT-US91-02714-24 (1-1276)
QY 29 GluGluGluGluGluProGluLeuSerProAlaaspAlaCysProLeuAlaGluLeuArg 48
Db 71 GAACCTATGGAGAGAGAGAGATTAAACCA----- 100
QY 49 AlaAlaGluLeuGluProValaGlyHisIstGlyGlnValaGluLeuThrGluThrSer--- 67
Db 101 -----CAAACTGAAGAGCACTATCAAAAGAAATTGCATC 136
QY 68 -----ValaasnValaGlyProGluArgIleGlyProHisCysPheGluLeuLeuArg 84
Db 137 ACACATCATGTAAAGAGACATGAAGAACGACATCTCCAGTTGAACCTTTAAAA 196
QY 85 ValLeuGluGlyGlyGlyGlyGlyGlyValaPheGlnValaArgGlyValaGlnGlyThrAsn 104
Db 197 GTATTAGGGCAGGATCATCTTTGGAAAGGTTTCTTGAATAAAATCTCAGGCTCGAT 256
QY 105 LeuGlyLysIleGlyAlaMetLysValLeuArgLysAlaLysIleValaArgAsnAlaLys 124
Db 257 GCTAGGCAGCTTTATGCCATGAGTATGAAGAGCCACATG-----AAAGTTGCA 310
QY 125 AspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPheIle 144
Db 311 GACCGAGTTCCGACAAAATGAACGTCATCTTGAGTAGAGATTAAATCATCTTTATAT 370
QY 145 ValGluLeuAlaTyThrAlaPheGlnThrGlyGlyLysLeuTyThrIleLeuGluCysLeu 164
Db 371 GTCAAGTTGCATTAATCT-TTTCAAACGTGAAGGAAAGTTGATCTTAT-TTGGAATTTCTC 428
QY 165 SerGlyGlyGluLeuPheThrHisLeuGluArgGlyGlyIlePheLeuGluAspThrAla 184
Db 429 AGGGAGAGAGATTGTTTACACGCTTATCCAAAGAGTGATGTCACGAAGAAGATGTC 488
QY 185 CysPheTyThrAlaGluIleThrLeuAlaLeuGlnHisLeuHisSerGlnGlyIleIle 204
Db 489 AAATCTACCTGCGTGAACCTTGCACTGCTTACACATCACTACCTGCGGATATAT 548
QY 205 TyThrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeuThr 224
Db 549 TATAGAGACTTAAACCGAAATATCTT-CTTGATGAAGAGCATCATCAAGTTAAACA 607
QY 225 AspPheGlyLeuGlyLysGluSerIleHisGluGlyAlaValaThrHisThrPheCysGly 244
Db 608 GATTTCGGCTTAAGTAAGAGATCTATTACCATGAAGAGGATATCT-TTTTGTCGA 666
QY 245 ThrIleGluTyThrMetAlaProGluIleLeuValaArgSerGlyHisAsnArgAlaVala 264
Db 667 ACTGGAGATATATGGCTCCAGAGTAGTATATCGTCGAGATCATACACAGAGCTGAC 726
QY 265 TyrTrpSerLeuGlyAlaLeuMetLysTrpMetLeuThrGlySerPro-ProPheThrAl 284
Db 727 TGGTGGCTTTTGGTGTGTATATGTTGAATGCTTACTGTGATCCACTCCCTTCCAAAG 786
QY 284 agLusnArgLysLysThrMetAspLysIleIleArgGly-LysLeuAlaLeuProprot 304
Db 787 AAAGATCAAAAGAAACAAATGACATGATCTTTAAACCAAACTTGAAATGCCACAGT 846
QY 304 TyLeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlna 324
Db 847 TTTTGAGTCTGTAAGCGCAGAGCTTTTACGAATGCTTTMAAGCGAAGATCTCGCAACA 906
QY 324 rglIleGlyGlyGlyProGlyAspAlaAlaaspValaGlnaArgHisProPheArgHisM 344
Db 907 GATTAGGTGACAGACACATGAGATTGAAGAAATTAAGAACATTCATTTTCTCAACGA 966
QY 344 etAsnTrpAspAspLeuLeuAlaTrpArgValaAspProPheArgProCysLeuGlns 364
Db 967 TAGACTGAATAACTGTATAGAGA-GAATTCATCCGCCATTTTAAACCTGCAACGGCA 1025
QY 364 ergluGluaspValserGlnPheaspThrArgPheThrArgGlnThrProValaspSerp 384
Db 1026 GGCCGTGAATACATCTTATTTTGTATCTGAGTTTACTGCAAAAACCTCCAAAGATTTCAC 1085

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 18, 2002, 20:55:41 ; Search time 2846 Seconds

(without alignments)
5061.802 Million cell updates/sec

Title: US-09-762-258-2
Perfect score: 2614
Sequence: 1 MARGRRARAGAAVAFDL.....PIRPSGTRKSKRGRRGR 495

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODELS=frame_p2n.model -DEV=xlh
-O=/cgn2_1/USFPO.spool/US09762258/runat_13112002_102448_5044/app.query.fasta_1.647
-DB=GenEmbl -GFM=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=Dlosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09762258_@CGN_1_1182_@runat_13112002_102448_5044 -MCP=6 -ICPU=3
-NO_XLPHY -NO_MMAB -LARGEQUERY -NES_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.*
1: gb_da.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_da.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*

29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rtd.*
36: em_htg_man.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2614	100.0	1735	9 AB016869	AB016869 Homo sapi
2	2605	99.7	1720	9 AF099739	AF099739 Homo sapi
3	2600	99.5	1807	9 BC000094	BC000094 Homo sapi
4	2594	99.2	1716	9 AF076931	AF076931 Homo sapi
5	2594	99.2	1732	6 AR206888	AR206888 Sequence
6	2586	98.9	1788	9 BC006106	BC006106 Homo sapi
7	2572.5	98.4	1744	9 AB019245	AB019245 Homo sapi
8	2364.5	90.5	1491	10 MM07938	AJ007938 Mus muscu
9	1749	66.9	1778	4 OCG3PK	X54415 Rabbit mRNa
10	1748	66.9	2346	6 AX333655	AX333655 Sequence
11	1748	66.9	2346	9 HUMP70S6RA	M60724 Human p70 r
12	1746	66.8	1800	10 RAT56KIN3	M57428 Rat S6 kina
13	1745	66.8	1791	9 HUMP70S6KB	M60725 Human p70 r
14	1740	66.6	2287	10 RAT56PK	M58340 Rat S6 prot
15	1692.5	64.7	1717	5 XLA131521	AJ131521 Xenopus l
16	1468	56.2	1775	3 AF282407	AF282407 Artemia f
17	1455	55.7	2556	6 A69489	A69489 Sequence 1
18	1455	55.7	2556	6 A72166	A72166 Sequence 1
19	1450	55.5	2399	3 DMU66562	U66562 Drosophila
20	1447	55.4	2481	3 AY095090	AY095090 Drosophila
21	1415	54.1	3479	3 AR086879	AR086879 Sequence
22	1385.5	53.0	1607	6 AF003419	AF003419 Homo sapi
23	1383	52.9	168567	9 AC005849	AC005849 Homo sapi
24	1383	52.9	169144	2 AC002437	AC002437 Homo sapi
25	1340	51.3	135116	2 AC109138	AC109138 Mus muscu
26	1271.5	48.6	269355	2 AF294915	AF294915 Aplysia c
27	1266.5	48.5	2770	6 AX250156	AX250156 Sequence
28	1211.5	46.3	843	2 AC014816	AC014816 Drosophila
29	1149	44.0	54667	2 AC010716	AC010716 Drosophila
30	1149	44.0	173588	3 AC093500	AC093500 Drosophila
31	1149	44.0	173558	3 AE003565	AE003565 Drosophila
32	1149	44.0	286583	3 CEY47D3A	AL117202 Caenorhab
33	1134	43.4	199814	3 BC005694	BC005694 Mus muscu
34	1032.5	39.5	1114	10 XLP70S6	X66179 X.laeyis p7
35	1005	38.4	663	5 BC014966	BC014966 Homo sapi
36	980.5	37.5	3206	5 AF165162	AF165162 Xenopus l
37	977	37.4	2214	5 M99169	M99169 Rat S6 prot
38	974	37.3	3131	10 RAT56KINX	AY409499 Sequence
39	966	37.0	3061	6 HUMS6KINA	L07597 Homo sapien
40	966	37.0	3061	3 AB073313	AB073313 Asterina
41	962.5	36.8	2382	3 MMU031021	AJ131021 Mus muscu
42	961.5	36.8	5240	10 AX019387	AX019387 Sequence
43	961	36.8	2791	6 HSRNARS6K	X85106 H.sapiens m
44	961	36.8	2791	9 HUMS6KINB	L07598 Homo sapien
45	960	36.7	1620	9	

RESULT 1

ALIGNMENTS

Qy 441 SerProhegiuglyPheargProSerProSerLeuProGluProThrGluLeuProLeu 460
Db 1336 TCCTTTTGAAGGGGTTTCGGGCCAGCCAGCTGCGGAGCCAGGAGGTACTCTA 1395
Qy 461 ProProLeuLeuProProProProSerThrThraProLeuProIleargProPro 480
Db 1396 CCTCACCTCTGCGCACCCCGCGCTCGACACCGCCCTCTCCATCCGTCGCCCC 1455
Qy 481 SerGlyThrLysSerLysArgGlyArgGlyArgProGlyArg 495
Db 1456 TCAGGACCAAGAGTCCAGAGGGCGTGGCGTCCAGGGCGC 1500
RESULT 2
AF099739 1720 bp mRNA linear PRI 24-NOV-2000
LOCUS Homo sapiens S6 kinase-related kinase mRNA, complete cds.
DEFINITION AF099739
ACCESSION AF099739.1 GI:4454856
VERSION
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Koh,H., Jee,K., Lee,B., Kim,J., Kim,D., Yun,Y.H., Kim,J.W.,
Choi,H.S. and Chung,J.
TITLE Cloning and characterization of a nuclear S6 kinase, S6
JOURNAL kinase-related kinase (SRK); a novel nuclear target of Akt
MEDLINE Oncogene 18 (36), 5115-5119 (1999)
PUBMED 10490846
REFERENCE 2 (bases 1 to 1720)
AUTHORS Koh,H.J., Lee,B.N., Choi,H.S. and Chung,J.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-1998) Biological Sciences, Korea Institute of
Advanced Science and Technology, Kusong, Yuseong, Taejon 305-701,
South Korea
FEATURES
source location/qualifiers
1..1720
/organism="Homo sapiens"
/db_xref="taxon:9606"
40..1488
/note="SRK; similar to ribosomal protein S6 kinase,
p70-S6k"
/codon_start=1
/product="S6 kinase-related kinase"
/protein_id="A4D20990.1"
/db_xref="GI:4454857"
/translation="MAAVFDLDELTEGSEGESEPELSPADACPLAEALRAAGLEPVH
YEEVELTETSYNNGPERIGPHCFELLEGCGGKGYKPOVKKQGTNIGKYAMKIVR
KAKIVRAKDPATNRARNTLESKHPFYELAYAFOTGKLYITILECLSGELFTHL
EREGIFLEDYACFTLAETITLALGHLHSOGIIYRLKRPENILMSOGHKLTFGLCKE
SINGAVYHFCGCIEMAPELIVRSQHRAVDMSLGALMYDMITGSPPTAENRK
TMDKIRGKLALPYLTPDAADLVKFKLRPSORIGSGPDADAVOHRPFRRNMND
DLAMRVDPFRPCLOSEEDVSDPTRTFTPTVDSDPTDRLSSANOAFLGPFYVAP
SVLDSTKEGFSPOKRLSPRLNSPPRVPVPLKFSPEEGRSPSLUPETIELPLPL
LPPEPSTIAPLPIRPPSGRTKSKRGRROR"
BASE COUNT 339 a 533 c 535 g 313 t
ORIGIN
Alignment Scores:
Pred. No.: 3,66e-134 Length: 1720
Score: 2605.00 Matches: 493
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.66% Indels: 0
Gaps: 0
US-09-762-258-2 (1-495) x AF099739 (1-1720)
Qy 3 ArgGlyArgArgAlaArgGlyAlaGlyAlaAlaMetAlaAlaValPheAspLeuAspLeu 22
|||||

Db 7 AGGGGCCAGCGGGCCCGGGGGCCGCCCGCCATGAGCGCCGTGTTGATTTGGATTGG 66
Qy 23 GluThrGluGluGlySerGluGlyGluGluGluProGluLeuSerProAlaAspLacys 42
Db 67 GAGACGAGAGAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 126
Qy 43 ProLeuAlaGluLeuAlaAlaAlaGlyLeuGluProValGlyHisTyrGluGluVal 62
Db 127 CCCCTTGGCGAGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 186
Qy 63 LeuThrGluThrSerValAsnValGlyProGluArgGlyGlyProHisCysPheGluLeu 82
Db 187 CTGACTGAGACCAAGCGCTACAGCTTGGCCAGAGCCATCGGGCCCATCGCTTTAGCTG 246
Qy 83 LeuArgValLeuGlyLysGlyGlyTyrGlyLysValPheGlnValArgLysValGlnGly 102
Db 247 CTGCGTGTGCTGGGCAAGGGGGGCTATGGCAAGGGTTCACAGTGCAGAAAGGTGCAAGGC 306
Qy 103 ThrAsnLeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsn 122
Db 307 ACCAACTGGGGCAAAATATATGCCATGAAGTCCTAAGGAAGGCCAAATTTGTGGCAAT 366
Qy 123 AlaLysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisPro 142
Db 367 GCCAAGGACACAGACACACACAGCGGCTGAGCGGAACATTCTAGACTGAGTGAACACCCC 426
Qy 143 PheIleValGluLeuAlaIleTyrAlaPheGlnThrGlyGlyLysLeuTyrLeuIleLeu 162
Db 427 TTTATTTGGGAACCTGGCTATGCTTCAGACTGGTGGCAAACTCTACCTATCTCTTAG 486
Qy 163 CysLeuSerGlyGlyLysLeuPheThrHisLeuGluArgGlyLysIlePheLeuGluAsp 182
Db 487 TCCTTCATGTTGGGAGGAGCTCTTCACGCATCTGGAGCGAGAGGAGATCTTCTGGAAAT 546
Qy 183 ThrAlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGly 202
Db 547 ACGGCTCTCTTACCTGAGTATGATGACGGCTGGGCGCATCTCCACCTCCAGGGGC 606
Qy 203 IleIleTyrArgAspLeuLysProGluAsnIleMetLysSerGlnGlyHisIleLys 222
Db 607 ATCATCTACCGGAGCTCAAGCCGAGAACATCATGCTCAGAGCGAGGCGCACATCAAA 666
Qy 223 LeuThrAspPheGlyLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPhe 242
Db 667 CTGACCGACTTTGGACTCTGCAAGAGCTATTCATGAGGGCGCGCTACATCACACCTTC 726
Qy 243 CysGlyThrIleGlyTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAla 262
Db 727 TCGGCGACCAATTGAGTATGATGCGCCCTGAGATTCTGTGGCAGTGGCCACACCGGGCT 786
Qy 263 ValAspTyrPyrPsrLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPhe 282
Db 787 GTGGAGCTGTGGAGCTGGGGGCTGTGATGATGACATGCTACATGATGCGCGCTTT 846
Qy 283 ThrAlaGluAsnArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuPro 302
Db 847 ACCGAGAGAACCGGAGAAACCAATGATTAAGATCATCAGGGGCAACTGGCACTGGCC 906
Qy 303 ProTyrLeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSer 322
Db 907 CCCCTACCTACCCCGAGATGCCCGGAGCTTGTCAAAAGTTTCTGAACGGAATGCCAGC 966
Qy 323 GlnArgIleGlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisProPheThrArg 342
Db 967 CAGCGAGATTGGGGGTGGCCAGAGGAGTCTGCTGATGTGCAAGACATCCCTTTTCCGG 1026
Qy 343 HisMetAsnTyrPsrAspLeuLeuAlaThrParGlyAlaAspProProPheArgProCysLeu 362
Db 1027 CACATGAATTTGGAGAGGAGCTTGGCTGGCTGTGGACCCCTTTACAGGCCCTGTCTG 1086
Qy 363 GlnSerGluGluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAsp 382
Db 1087 CAGTCAGAGAGAGAGCTGAGCCAGTTTGATACCCGCTTCACACGCGCAGACGCGGTGGAC 1146

QY 383 SerProAspThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTyr 402
| | | | |
Db 1147 AGCTCGATGACACAGCCCTCAGCAGAGAGCCACACAGCCCTCTCGGCTTACATAC 1206
| | | | |
QY 403 ValAlaProSerValLeuAspSerIleValGlyPheSerPheGlnProIleValArg 422
| | | | |
Db 1207 GTGGCCCGCTGTCTGTGACACATCAAGAGGGCTTCTCTCCAGCCCAAGCTGGCG 1266
| | | | |
QY 423 SerProArgArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerPro 442
| | | | |
Db 1267 TCACCCAGCGGCTCAACAGTACCCCGGGGTCCCGCTCAGCCCTCAAGTTCTCCCT 1326
| | | | |
QY 443 PheGluGlyPheArgProSerProSerLeuProGluProThrGluLeuProLeuProPro 462
| | | | |
Db 1327 TTTCAGGGGTTTCGGCCAGCCAGCTGCGAGCCAGCAGGAGTACTTCACTTCA 1386
| | | | |
QY 463 LeuLeuProProProProProSerThrThrAlaProLeuProLeuArgProProSerGly 482
| | | | |
Db 1387 CTCTCTCCACCGCGCGCGCTGACCCAGCCGCTCTCCCTCCCTCCCTCAGG 1446
| | | | |
QY 483 ThrLysLysSerLysArgGlyArgGlyArgProGlyArg 495
| | | | |
Db 1447 ACCAAGATGCAAGAGGGCGCTGGCGCTCCAGGGCGC 1485
| | | | |
RESULT 3
BC000094 1807 bp mRNA linear PRI 12-JUL-2001
LOCUS Homo sapiens, ribosomal protein S6 kinase, 70kd, polypeptide 2,
DEFINITION clone MGC:1848 IMAGE:3508140, mRNA, complete cds.
ACCESSION BC000094.1 GI:12652690
VERSION BC000094.1 GI:12652690
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1807)
Strausberg, R.
Direct Submission
Submitted (03-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbioology.org>
Contact: amadansystemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Kettman and Anuradha Madan
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 7 Row: h Column: 4
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4165310.
FEATURES
source
1..1807
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="locusid:6199"
/db_xref="taxon:9606"
/clone="MGC:1848 IMAGE:3508140"
/tissue_type="Brain, neuroblastoma"
/clone_lib="NIH-MGC_19"
/lab_host="DH10B-R"
/note="Vector: pORF7"
65..1513
/codon_start=1

/product="ribosomal protein S6 kinase, 70kd, polypeptide
2"
/protein_id="AAH00094.1"
/db_xref="gi:12652691"
/translation="MAVFDLDLEPESSEGEPELSPADACPLAELRAGLEPVGH
YREVELTETSVAVGPERIGPHCFELLRLVLGKGQYKRVQSTNGKITYAMVLR
KAKIVRNKADTAHTAEIRNLESVNHPTVELAIVFOTGGKLYLTLELSEGLFTIL
EREGLFEDTACEYLAETTLAHLHSGIYTRDKPENIMLSGHLKTFDGLCKE
SIHEGAVHTFCGTYEYMAPELLVRSGNRAVDWMSLGALMDLTGSPPTAENRK
TMDKIRKRLALPYLTEDARDLVKFLKRNPSORIGGPDGAPDAVORHPFERNMD
DLAMRVDPPEPFCLOSEEDYSQFTRTROTVPDPSDDTALSESANQAPFGFTYAP
SVLDSIKGEFSQPKLRSPRRNLSPPRPVPSPLKSPFEGFRPSLSLEPFIPLPLPL
LPPEPSTTAPLPIPPSGTKSKRGKRPGR"
BASE COUNT 405 a 540 c 545 g 317 t
ORIGIN
Alignment Scores:
Pred. No.: 7,23e-134 Length: 1807
Score: 2600.00 Matches: 492
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.46% Indels: 0
DB: Gaps: 0
US-09-762-258-2 (1-495) x BC000094 (1-1807)
QY 4 GlyArgArgAlaArgLysAlaGlyAlaAlaMetAlaAlaValaPheAspLeuGlu 23
| | | | |
Db 35 GCGCCAGCGGGCG 94
| | | | |
QY 24 ThrGluGluGlySerLysLysLysLysLysLysLysLysLysLysLysLysLys 43
| | | | |
Db 95 ACGGAGAAAGCGACGAGGCGCGAGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 154
| | | | |
QY 44 LeuAlaGluLeuArgAlaAlaGlyLeuGluProValaGlyHisTyrGluValaGlu 63
| | | | |
Db 155 CTTCGCGAGTTGAGGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 214
| | | | |
QY 64 ThrGluThrSerValAsnValaGlyProGluArgIleGlyProHisCysPheGluLeu 83
| | | | |
Db 215 ACTGAGACGACGCGTGAACGTGGCCAGAGCGCATGCGGCGCGCGCGCGCGCGCG 274
| | | | |
QY 84 ArgValLeuGlyLysGlyLysGlyLysValaPheGlnValaArgLysValaGlnGly 103
| | | | |
Db 275 CGGTCTCTGGCAAGGCGGCGTATGCAAGGTCTTCAGGTGGCAAGGTGCAAGC 334
| | | | |
QY 104 AsnLeuGlyLysIleThrAlaMetLysValaLeuArgLysAlaLysIleValaArg 123
| | | | |
Db 335 AACTGGGCAAAATATATGCGCATGAAGATCTTAAGAGAGGCCAAATTTGCGCA 394
| | | | |
QY 124 LysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValaLysHisPro 143
| | | | |
Db 395 AAGGACACAGCACACACAGCGGCTGAGCGGAACATTCTAGAGTCAATGAAGC 454
| | | | |
QY 144 IleValGluLeuAlaTyrAlaPheGlnThrGlyLysLeuTyrIleuLeuGluCys 163
| | | | |
Db 455 ATGTGGAAGTGGCTATGCTTCCAGACTGGGCAAACTCACTCACTTGGTGGTGC 514
| | | | |
QY 164 LeuSerGlyGlyValLeuPheThrHisLeuGluArgGlyGlyIlePheLeuGluAsp 183
| | | | |
Db 515 CTGAGTGGTGGAGGCTCTTCAAGCATCTGGAGCGAGAGGCACTTCTCGGAAGT 574
| | | | |
QY 184 AlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGly 203
| | | | |
Db 575 GCGTGTCTTACTGCTGATGATCAAGCGCGCGCTGGCGCATCTCCAGCGGCA 634
| | | | |
QY 204 IleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLys 223
| | | | |
Db 635 ATCTACCGGAGACTCAAGCCGAGAACATCAGTCAGCAGCGGCGGCAATCAAC 694
| | | | |
QY 224 ThrAspPheGlyLeuGlyLysGlySerIleHisGlyValaValaThrHisThrPhe 243
| | | | |
Db 695 ACCGACTTGTGACTGTGCAAGAGTCTATCCATGAAGGCGCGCTCACTACACCTT 754
| | | | |

QY 244 GlyThrIleGlyMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaVal 263
 |||||
 Db 755 GGACACATGAGTACATGAGCCCTGAGATTCTGGCCCACTGGCCACACCGGGCTGTG 814
 QY 264 AspTrpTrpSerLeuGlyAlaLeuMetGlyAspMetLeuThrGlySerProPheThr 283
 |||||
 Db 815 GACTGGTGGAGCTGGGGGCGCTGATGTAGACATGCTCACTGGATGGCGCCCTTAC 874
 QY 284 AlaGluAsnArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuPro 303
 |||||
 Db 875 GCAGAGAACCCGAGAAACCATGATGATCATCAGGGGCAAGCTGGCACTGCCCC 934
 QY 304 TyrLeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAspSerGln 323
 |||||
 Db 935 TACCTACCCAGATGCCCGGACCTGTCTCAAAAGTTTCTGAACCGGAATCCAGCCAG 994
 QY 324 ArgIleGlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHis 343
 |||||
 Db 995 CGGATGGGGGTGGCCGAGGGGATGCTGCTGATGGCAGACATCCCTTTTCCGGCAG 1054
 QY 344 MetAsnTrpAspAspLeuAlaTrpArgValAspProProPheArgProCysLeuGln 363
 |||||
 Db 1055 ATGAATTGGACGACCTTCTGCTGGCTGGAGTGGACCCCTTCAGGCGCTGCTGCAG 1114
 QY 364 SerGluGluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSer 383
 |||||
 Db 1115 TCAGAGGGAGCGTGAAGCCATTTGATACCCGCTTCACAGGACGCCGCTGGACAGT 1174
 QY 384 ProAspAspThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTyrVal 403
 |||||
 Db 1175 CCTGATGACACAGCCCTCAGGAGAGTGCACACAGGCTTCCTGGGCTTCACATACGTG 1234
 QY 404 AlaProSerValLeuAspSerIleLysGluLysPheSerPheGlnProLysLeuArgSer 423
 |||||
 Db 1235 GCGCGCTGTCTCGAGACATCAAGAGAGGCTTCTTCACAGCCCAACCTGGCGTCA 1294
 QY 424 ProArgArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerPhePhe 443
 |||||
 Db 1295 CCCAGGCGCTCAACAGTACGCCCGGCGGTCCCGCTCACGCCCTCAATCTCCCTTTT 1354
 QY 444 GluGlyPheArgProSerProSerLeuProGluProThrGluLeuProLeuProLeu 463
 |||||
 Db 1355 GAGGGGTTCGGCCAGCCCGACGCTCGGAGCCAGGAGTACCTTACCTCCACTC 1414
 QY 464 LeuProProProProProSerThrThrAlaProLeuProIleArgProProSerGlyThr 483
 |||||
 Db 1415 CTGCCACCGCGCGCTTCACACACCGCCCTCTCCCATCCGCTCCCTCAAGGAGC 1474
 QY 484 LysLysSerLysArgLysArgLysArgProGlyArg 495
 |||||
 Db 1475 AAGAGTCCAAAGAGGGCGTGGCGTCCAGGGCGC 1510
 RESULT 4
 AF076931 1716 bp mRNA linear PRI 24-NOV-2000
 LOCUS Homo sapiens serine/threonine kinase 14 beta (STK14B) mRNA,
 DEFINITION complete cds.
 ACCESSION AF076931
 VERSION AF076931.1 GI:5668906
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 1716)
 AUTHORS Lee-Fruman,K.K., Kuo,C.J., Lipincott,J., Terada,N. and Blenis,J.
 TITLE Characterization of S6K2, a novel kinase homologous to S6K1
 JOURNAL Oncogene 18 (36), 5108-5114 (1999)
 MEDLINE 99422045
 PUBMED 10490847
 REFERENCE 2 (bases 1 to 1716)
 AUTHORS Lee-Fruman,K.K., Kuo,C.J., Lipincott,J., Terada,N. and Blenis,J.

TITLE Direct Submission
 JOURNAL Submitted (06-JUL-1998) Cell Biology, Harvard Medical School, 240
 Longwood Ave., Boston, MA 02115, USA
 FEATURES
 source
 1. 1716
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="11"
 /map="11q13"
 /cell_type="Jurkat T cell"
 1. 1716
 /gene="STK14B"
 35. 1484
 /gene="STK14B"
 /note="similar to p70 S6 kinase; kinase-like S6 kinase;
 KLS"
 /codon_start=1
 /product="serine/threonine kinase 14 beta"
 /protein_id="AA046063.1"
 /db_xref="GI:5668907"
 /translation="MAVFDLDLETGSGEGPELSPADCPLELRAGLEPVGH
 YEVELETISVNVGPERIGPHCELELVLEKGGYGVQVRKVGNTLGIYAMKYL
 KAKIVRNADPTAHTRARNTLESYKHPFIVELAYAFQTGKLYLILECSGELFTHL
 ERGRIPLIEDPACFYLAITLALGHSGIITVDIKPENITLSSGHTIKLDPGLKE
 SIHGAVTHFFRCGTEYMAPELIVRSNGNVAWMSIGALMYMLTSGPPTAENRK
 TMKTIIRKIALPPVLPDPAADLYKRIKRNPSORIGCGDAADVQRRHFFPHMND
 DLAMRVDPFPRCLQSEEDVSDRTIRFTQTPVDSFDTLASESANQAFLTFTYAP
 SVLDISIKGFSFQPKLSPRRLNSPPVSPKLFSPFEGFRSPSLPEPTLPLPL
 LPPPTPTAPLPIRPSGTRKSRGRGRGR"
 BASE COUNT 339 a 532 c 532 g 313 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.46e-133 Length: 1716
 Score: 2594.00 Matches: 491
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.23% Indels: 0
 DB: Gaps: 0
 US-09-762-258-2 (1-495) x AF076931 (1-1716)
 QY 5 ArgArgAlaArgGlyAlaGlyAlaAlaMetAlaAlaValPheAspLeuAspLeuThr 24
 |||||
 Db 9 CGACGGGCGCCCGGGCGCGCGCCCGCATGCGCGCGCTGTGATTTGATTTGGAGACG 68
 QY 25 GluGluGlySerGluGlyGluGluProGluLeuSerProAlaAspAlaCysProLeu 44
 |||||
 Db 69 GAGGAAGGCACGAGAGGGGAGGAGGAGCAGAGCTACGCCCGGGGAGCAGTGCCTT 128
 QY 45 AlaGluLeuArgAlaAlaGlyLeuGluProValGlyHisTyrGluGluValGluLeuThr 64
 |||||
 Db 129 GCCGAGTTGAGGCGAGCGGCGCTGAGACCTGTGGACACTAGAAAGAGTGGAGCTGACT 188
 QY 65 GluThrSerValAsnValGlyProGluArgIleGlyProHisCysPheGluLeuLeuArg 84
 |||||
 Db 189 GAGACACCGTGAAACGTTGGCCGAGCGCATTCGGGCCCATCTGTTGACCTGCTGCT 248
 QY 85 ValLeuGlyLysGlyGlyTyrGlyLysValPheGlnValArgLysValGlnGlyThrAsn 104
 |||||
 Db 249 GTGCTGGCGCAAGGGGGCTATGGCAAGTGTCCAGGTGCCAAAGAGTCCAAAGCACCAC 308
 QY 105 LeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLys 124
 |||||
 Db 309 TTGGGCAAAATATATGCCATGAAAGTCTTAAGAAAGCAAAATTTGCGCAATGCCAAG 368
 QY 125 AspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPheIle 144
 |||||
 Db 369 GACACAGACACACAGCGGCTGAGCGGAGAACATTTAGAGTARGTAAAGACACCTTTATT 428
 QY 145 ValGluLeuAlaTyrAlaPheGlnThrGlyLysLysLeuTyrLeuIleLeuGluCysLeu 164
 |||||
 Db 429 GTGGAAGTGGCTTATGCTTCACAGCTGTGGCAAAACTTACCTCATCTTGAAGTGCCTC 488

QY 165 SerGlyGlyGluLeuPheThrHisLeuGluArgGlyIlePheLeuGluAspThrAla 184
DB 489 AGTGGTGGGAGAGCTTTCACAGCATCTGGAGCGAGAGGAGCATCTTCTGGAAAGATACGGCC 548
QY 185 CysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleLe 204
DB 549 TGGCTTACCTGGCTGAGATCAACGCTGGCCCTGGCCATCTCCACTCCACAGGAGCATATC 608
QY 205 TyrArgAspLeuAspProGluAsnIleMetLeuSerSerGlnGlyHisIleTyrLeuThr 224
DB 609 TACCGGAGCTCAAGCCCGAAGAACATCATGCTCAGCAGCGAGGCGCACATCAACAGCAGC 668
QY 225 AspPheGlyLeuCysGlySerIleHisGluGlyAlaValThrHisThrPheCysGly 244
DB 669 GACTTTGAGCTCTGCAGAGAGTCTATCATGAGGCGCGCTCACTCAACCTTCTCGCGC 728
QY 245 ThrIleGlyTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAsp 264
DB 729 ACCATTGAGTACATGGCCCTTGAGATTCTGTGGCAGTGGCCACAAACGGGCTGTGGAC 788
QY 265 TyrTrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThrAla 284
DB 789 TGGTGGAGCTGGGGGCGCTGATGATGACATGCTCACTGATGAGCGCGCTTTACCGCA 848
QY 285 GluAsnArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProProTyr 304
DB 849 GAGAACCGGAGAAACCATGATGATCATCAGGGGCAAGCTGGCAGCTGCCCTTAC 908
QY 305 LeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArg 324
DB 909 CTCACCCCAAGATGCCCGGAGCTTGTCAAAATTTCTGAACGGAATCCACCGAGCG 968
QY 325 IleGlyGlyLysProGlyLysAspAlaIleAspValGlnArgHisProPheArgHisMet 344
DB 969 ATTGGGGGGTGGCCAGGAGATGCTGTGATGTCAGAGACATCCCTTTTCCGGCAGAG 1028
QY 345 AsnTrpAspAspLeuAlaTrpArgValAspProProPheArgProCysLeuGlnSer 364
DB 1029 AATTGGGAGAGACTTCTGCGCTGTGGACCCCTTTCAGCGCTGTGTGACATCA 1088
QY 365 GluGluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSerPro 384
DB 1089 GAGGAGAGCTGAGCCAGTTGATACCCCTTTCACAGCGAGCGCGGGTGGACATCTCT 1148
QY 385 AspAspThrAlaLeuSerGlnSerAlaAsnGlnAlaPheLeuGlyPheThrTyrValAla 404
DB 1149 GATGACACAGCCCTGACGAGATGCCAACAGCCCTTCTCGGGCTTCACATACGTGGCG 1208
QY 405 ProSerValLeuAspSerIleLysGluGlyPheSerPheGlnProLysLeuArgSerPro 424
DB 1209 CCGTCTGTCTGGACATCAAGAGGAGGCTTCTCTTCAGCCCAAGCTGCGCTCACCC 1268
QY 425 ArgArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerProPheGln 444
DB 1269 AGCGGCTCAACAGTACGCCCGGGGTCCCGGTAGGCCCTCAAGTCTTCTCTTTGAG 1328
QY 445 GlyPheArgProSerProSerLeuProGluProThrGluLeuProLeuProProLeuLeu 464
DB 1329 GGGTTTGGGCGGAGCCGAGCGCTGGGAGCCAGGAGAGTACTTACTTCCACTCCCTG 1388
QY 465 ProProProProProSerThrThrAlaProLeuProIleArgProProSerGlyThrLys 484
DB 1389 CCACCCCGCCCGCTTCGACACACCGCCCTTCCATCCGCTCCCGCTCAGGAGCAAG 1448
QY 485 LysSerLysArgGlyArgGlyArgProGlyArg 495
DB 1449 AAGTCCAAAGAGGGCGGTGGCGCTCCAGGGCGC 1481
RESULT 5
LOCUS AR206888 1732 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 1 from patent US 6372467.

ACCESSION AR206888 GI:21505626
VERSION AR206888.1
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1732)
AUTHORS Blenis,J., Lee-Fruman,K.K. and Kuo,C.J.
TITLE p546k and p856k genes, proteins, primers, probes, and detection methods
JOURNAL Patent: US 6372467-A 1 16-APR-2002;
FEATURES
source location/Qualifiers
BASE COUNT 355 a 532 c 532 g 313 t
ORIGIN
Alignment Scores:
Pred. No.: 147e-133 Length: 1732
Score: 2594.00 Matches: 491
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.23% Indels: 0
DB: 6 Gaps: 0
US-09-762-258-2 (1-495) x AR206888 (1-1732)
QY 5 ArgArgAlaArgGlyAlaGlyAlaAlaMetAlaAlaValPheAspLeuAspLeuThr 24
DB 9 CGAGGGGCGCGCGGCG 68
QY 25 GluGluGlySerGluGlyGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 44
DB 69 GAGGAGGCGAGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAG 128
QY 45 AlaGluLeuArgAlaAlaLeuGluGluGluGluGluGluGluGluGluGluGluGluGlu 64
DB 129 GCCGAGTTAGGGCAGCTGCGCTGAGAGCTGTGGACACTATGAAAGGAGTGGAGCTGACT 188
QY 65 GluThrSerValAsnValAlaGlyProGluArgIleGlyProHisCysPheGluLeuLeuArg 84
DB 189 GAGACGAGGCTGACACTTGGCCAGAGCGCATTCGGGCCACTGCTTGAAGCTGGCGCT 248
QY 85 ValLeuGlyLysGlyLysIleGlyLysValPheGlnValArgLysValGlnGlyThrAsn 104
DB 249 GTGCTGGCAAGGGGGGCTATGGCAAGGTGTTCAGAGTCCGAAAGCTGCAAGGCAACAC 308
QY 105 LeuGlyLysIleThrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLys 124
DB 309 TTGGGCAAAATATATGCTCAAGAAAGTCTTAGAGAAAGCCAAATTTGGCAATGGCAAG 368
QY 125 AspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPheIle 144
DB 369 GACACAGCACACACAGGGGCTGAGCGGAACATTTCTAGTACAGTGAAGACCCCTTAT 428
QY 145 ValGluLeuAlaThrAlaPheGlnThrGlyGlyLysLeuTyrLeuIleLeuGluCysLeu 164
DB 429 GTGGAAGTGGCCATATGCTTCCAGAGTGGTGGCAAACTACTTACTTCACTTGAAGTCCCT 488
QY 165 SerGlyGlyGluLeuPheThrHisLeuGluArgGlyIlePheLeuGluAspThrAla 184
DB 489 AGTGGTGGGAGCTTTCACAGCATCTGGAGCGAGAGGAGATCTTCTGGAAAGTACGGCC 548
QY 185 CysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleLe 204
DB 549 TGGCTTACCTGGCTGAGATCAACGCTGGCCCTGGCCATCTCCACTCCACAGGAGCATATC 608
QY 205 TyrArgAspLeuAspProGluAsnIleMetLeuSerSerGlnGlyHisIleTyrLeuThr 224
DB 609 TACCGGAGCTCAAGCCCGAAGAACATCATGCTCAGCAGCGAGGCGCACATCAACAGCAGC 668
QY 225 AspPheGlyLeuCysGlySerIleHisGluGlyAlaValThrHisThrPheCysGly 244

Db	669	GACCTTGACCTCTGCAAGAGCATCTATTCATGATGAGGGCGCCGCTACCTACCTCTTCGCGC	728
Qy	245	ThrIleGlyIyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAsp	264
Db	729	ACCATTTGAGTACATGAGCCCTTGAGATCTCGGAGCCATGGCCACCAACGGGAGCTTGAC	788
Qy	265	TrpTrpSerLeuGlyAlaLeuMetIyrTrsPheLeuThrGlySerProProPheThrAla	284
Db	789	TGGTGAGACCTGGGGGCGCTCATGTACACATGCTCATGATGATGCGCCGCTTAAACC	848
Qy	285	GluAsnArgLysLysThMetAspLysIleIleArgGlyLysLeuAlaLeuProProIyr	304
Db	849	GAGAAACGGGAAGAAACCATGATGATTAAGTTCATCAGGGGCAAGCTGCACTGCCCCCTTAC	908
Qy	305	LeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArg	324
Db	909	CTCACCCAGATATGCCCGGGAGCTTGTCAAAAAGTTTGTGAACGGAAATCCAGCAGCGG	968
Qy	325	IleGlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMet	344
Db	969	ATTGGGGGTGGCCCAAGGGATGCTGCTCATGTGCAAGACATCCCTTTTCCGGCACATG	1028
Qy	345	AsnTrpAspAspLeuLeuAlaTrpArgValAspProProPheArgProCysLeuGlnSer	364
Db	1029	AATTGGAGCAGACTTCTTGCGCTGCGGTGTGACACCCCTTTTCAGGCGCTGTCTGACATCA	1088
Qy	365	GluGluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSerPro	384
Db	1089	GAGGAGGAGCAGTACCATTTGATATACCCGCTTACACAGGAGCGCGGTGGACAGTCTCT	1148
Qy	385	AspAspThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTyrValAla	404
Db	1149	GATGACACAGGCTTCAGGAGAGTCCCAACAGGCGCTTCGGGGCTTCACATACCTGCGC	1208
Qy	405	ProSerValIleAspSerIleLysGluGlyPheSerPheGlnProLysLeuArgSerPro	424
Db	1209	CCGTGTGTCCTGAGCAGCATCAAGAGGGCTTCTCTTCCAGCCCAACCTGCGCTCACCC	1268
Qy	425	ArgArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerProPheGlu	444
Db	1269	AGGCGCCTCAACAGTAGGCCCGGGGTCCCGACAGCCCTTCAAGTTCTCCCTTTTGAG	1328
Qy	445	GlyPheArgProSerProSerLeuProGluProThrGluLeuProLeuProProLeuLeu	464
Db	1329	GGGTTTCGGCCAGCCAGCTGCCGGAGGCCACGAGGATCACTCTACCTCACCTCTCG	1388
Qy	465	ProProProProProSerThrThrAlaProLeuProIleArgProProSerGlyThrLys	484
Db	1389	CCACGCCGCGCGCTTCACCAACGCGCCCTCTCCCATTCGTCCTCCCTCAGGAGCCAAAG	1448
Qy	485	LysSerLysArgGlyArgGlyArgProGlyArg	495
Db	1449	AAGTCCAGAGAGGCGCGTGGCGTCCACAGGGCGC	1481
RESULT 6			
LOCUS	BC006106	1788 bp	mRNA
DEFINITION	Homo sapiens, clone MGC:12950	IMAGE:2959036, mRNA, complete cds.	PRI 12-JUL-2001
ACCESSION	BC006106		
VERSION	BC006106.1	GI:13543927	
KEYWORDS	MGC.		
SOURCE	Homo sapiens.		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Strausberg,R.		
TITLE	Direct Submissiion		
JOURNAL	Submitted (02-APR-2001) National Institutes of Health, Mammalian		
	Gene Collection (MGC), Cancer Genomics Office, National Cancer		
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		
	USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		

COMMENT

Contact: MGC help desk
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: Louis B. Staudt, M.D., Ph.D.
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guln,
Leticia Hsiao, Martin Krzywnski, Reta Kutscher, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Llisa Prabhu, Parvaneh Saeedi, Jacqueline
Schell, Duane Smalius, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 18 Row: A Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction.

FEATURES

SOURCE	Location/Qualifiers
CDS	1..1788 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="MGC:12950 IMAGE:2959036" /tissue_type="Lymph, Burkitt lymphoma" /clone_lib="NIH_MGC_8" /_lab_host="DH10B-R" /note="Vector: pOTB7" 39..1487 /codon_start=1 /product="gunkun (protein for MGC:12950)" /protein_id="AAH06106.1" /_db_xref="GI:13543928" /translation="MAAFVDLDLTLEEGSEGEPELSPADACPLAEIARAAGLEPVGH YEVELETSTVNVGPERIGPSPFELLTVLGSGKGYOVAKVOGTMGIRYAMKVLR KAIIVRNADPTAHRARBNILIESVKHPFYELAYAPQTGGELYILECLSGELLETL ERKEFILEDTPACFPYLAEITLGLHSOGIIYRDLKPENMLISGOHIKITDELCKE SIHGCAVTHTPCGTIEYMAREPILYRSCHNRANVDWMSIALKATMDLPSSPPETANKRK TMDDITNGKLALPRPLYIPDARDADVLTKTELRNPSCRGEDRADVDVRHFPRIMND DLLAMRVDPFRPCLOSIEDVSQDFDTFTRTCPVSDSDPALSESANAQLGFYYAP SVLDISEGFSFOPKLRPSRLNSPPAPVPSPLFESFEGRFPSUPEPTELPLRPPL LPPEPSTMTALPRPPSGTRKSRRGRCPCR"

BASE COUNT 401 a 539 c 535 g 313 t

ORIGIN

```

Alignment Scores:
Pred. No.:          4,17e-133           Length:         1788
Score:              2586.00             Matches:          490
Percent Similarity: 99.59%               Conservative:     0
Best Local Similarity: 99.59%            Mismatches:       2
Query Match:        98.93%                Indels:           0
DB:                  Gaps:                 0

US-09-762-258-2 (1-495) x BC006106 (1-1788)
```

4 GTATGATGAATATGCTGTAAGAATAAACATCATTTCATTTGATTTTGCGAG 23
Db | |||||
9 GGCCACAGCGGCCGGCGGGCCCCGCCCAAGCGCGCGCTGTTCATTTGATTTTGCGAG 68
Db | |||||
24 ThringugluglySerGlUGlYGluGlyGuPrProGluUleUserProAlaAspaLaCyPro 43
Db | |||||
69 AGGAGGAAAGGAGCGAGAGGCGAGGCGAGCGACTCAGCCCCGCGAGCGCATGTCCC 128
Db | |||||

44 LeuaAtJuleArGaLAaAgLyueclUpProVaLglYlnStyrglGUvaLgIUeu 63
Db | |||||

129 CTTCGCGAGTTTAGGGCACGTGCGCTTAGAGCTGTGGGACACTATGAGAGAGTGAGCTG 188
Db | |||||

64 ThrGluTrSerValAsnaValcylPrProGUarGlileGlyPrOHnIsCysPhceLUdeUen 83
Db | |||||

Db 189 ACTGACACCAAGCTGACCTGGCCCAAGCCGATCGGGCCCTTGTAGCTGCTG 248
 Qy ArgValLeuGlyLysGlyGlyTyrGlyLysValPheGlnValArgLysValGlnGlyThr 103
 Db 249 CGTGTCTGGGCAAGGGGGGCTATGGCAAGGTCTTCAGGTGGCAAGGTCCAGGACAC 308
 Qy 104 AsnLeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAla 123
 Db 309 AACTTGGGCAAAATATATGATGCATGAAGATCTTAAGAGAGCCCAAAATTTGGCCAAATGCC 368
 Qy 124 LysAspThrAlaIleThrArgAlaGluArgAsnIleLeuGlnSerValLysHisProPhe 143
 Db 369 AAGGACACACGACACACAGGGCTGAGCGAATCTTGAAGTGAAGGACACCCCTTT 428
 Qy 144 LLevalGluLeuAlaTyrAlaPheGlnThrGlyLysLeuTyrLeuIleLeuGlnLys 163
 Db 429 ATGTGTGAAGTGGCTATGCTTCCAGAGCTGGTGGCAACTCACTCACTCACTCACTGATGC 488
 Qy 164 LeuSerGlyGlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThr 183
 Db 489 CTCAGTGGTGGCAGCTCTTACGATCTGACGAGGAGGAGGCTCTTCTGGAAGATACG 548
 Qy 184 AlAcysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIle 203
 Db 549 GCTTGCTTCTACCTGGCTGATGATCAGCTGGCCCTGGCCATCTCCACTCCAGGGCATC 608
 Qy 204 IleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeu 223
 Db 609 ATCTACCGGGACCTCAAGCCCGAGAACATCATCTCAGCAGGAGGCGCCATCAAACTG 668
 Qy 224 ThrAspPheGlyLeuLysLysGlnSerIleHisGlyAlaValThrHisThrPheCys 243
 Db 669 ACCGACTTTGGACTCTGCAAGAGTATATCCAGAGGGGCGCTCCTCACCTCTGTC 728
 Qy 244 GlyThrIleGluTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaVal 263
 Db 729 GGCACCATTTAGATACATGGCCCTGAGATTTCTGTGCGCAGTGGCCACAAACCGGCTGTC 788
 Qy 264 AspTrpTrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThr 283
 Db 789 GACTGGTGGAGCCTGGGGGCGCTGATGTAGACATCTCCTGATGGCGCGCCCTTACAC 848
 Qy 284 AlaGluAsnArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProPro 303
 Db 849 GCGAGAACCGGAGAAACCATGATGATATCAGGGGCAAGCTGGCAGTGGCCCGCC 908
 Qy 304 TyrLeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGln 323
 Db 909 TACCTACCCCAAGATCCCGGAGCTTGTCAAAAAGTTTCTGAAGAGGAATCCACACGAC 968
 Qy 324 ArgIleGlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisPheProPheArgHis 343
 Db 969 CGGATTTGGGGTGGCCAGGGGAGTCTGCTGATGTGACAGACATCCCTTTTCCGGCAC 1028
 Qy 344 MetAsnTrpAspAspLeuLeuAlaTyrPargValAspProProPheArgProCysLeuGln 363
 Db 1029 ATGAATTTGGACACCTTCTGGCGCTGGCTGGACCCCTTTCAGGGCCCTCTGCGAC 1088
 Qy 364 SerGluGluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSer 383
 Db 1089 TCGAGAGAGAGCTGAGCCAGTTGATACCCGCTTACACAGGAGAGAGCGCGGTGGACAGT 1148
 Qy 384 ProAspAspThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTyrVal 403
 Db 1149 CCGATGATGACACAGCCTTCAAGCAGAGATGCCAACAGGCGCTTCTGGGCTTCAATACATGCTG 1208
 Qy 404 AlaProSerValLeuAspSerIleLysGlyLysPheSerPheGlnProLysLeuArgSer 423
 Db 1209 GCGCCCTCTGCTCTGACAGCATCAAGAGGGGCTTCTCTCCAGCCCAAGGCTGCGCTCA 1268
 Qy 424 ProArgArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerProPhe 443
 Db 1269 CCCAGGCGCTCAACAGTACGCCCGCGGGCCCGCGTCAAGCCCTCAAGTTCTCCCTTTT 1328

Qy 444 GluGlyPheArgProSerProSerLeuProGluProThrGluLeuProLeuProProLeu 463
 Db 1329 GAGGGGTTTCGGGCCAGCCCAAGCTGCGGAGCCACAGGAGAGTACTTACTTCACTC 1388
 Qy 464 LeuProProProProProSerThrThrAlaProLeuProIleArgProProSerGlyThr 483
 Db 1389 CTGCCACCGCCCGCCCTTCGACACAGCCCGCTCTCCATCCATCCCTCCCTCAGGACG 1448
 Qy 484 LysLysSerLysArgGlyArgGlyArgProGlyArg 495
 Db 1449 AAGAACTCCAAGAGGGGCGCTGGGCTCCAGGGCGC 1484

RESULT 7
 AB019245 1744 bp mRNA linear PRI 06-FEB-1999
 LOCUS Homo sapiens p70 S6Kb mRNA for S6 kinase b, complete cds.
 DEFINITION
 ACCESSION AB019245.1 GI:4165310
 VERSION AB019245.1
 KEYWORDS p70 S6Kb; S6 kinase b.
 SOURCE Homo sapiens cell_line:erythrocyte leukemia cell CDNA to mRNA.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Salton,M., ten Dijke,P., Miyazono,K. and Ichijo,H.
 TITLE Cloning and characterization of p70(S6K beta) defines a novel family of p70 S6 kinases
 JOURNAL Biochem. Biophys. Res. Commun. 253 (2), 470-476 (1998)
 MEDLINE 99097259
 REFERENCE
 AUTHORS Salton,M. and Ichijo,H.
 TITLE Direct Submission
 JOURNAL Submitted (27-OCT-1998) Masao Salton, Tokyo Medical and Dental Univ., Dept. of Biomaterials Science, Faculty of Dentistry, 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8549, Japan (E-mail:msalton-indemuln.ac.jp, Tel:+81-3-5803-5473, Fax:+81-3-5803-0192)

FEATURES

source
 1..1744
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_line="erythrocyte leukemia cell"
 1..1744
 /gene="p70 S6Kb"
 53..1498
 /gene="p70 S6Kb"
 /codon_start=1
 /product="S6 kinase b"
 /protein_id="BA37145.1"
 /db_xref="GI:4165311"
 /translation="MAAVFDLLETEGSEGESEBELSPADACPLAELRAAGLEPVGH
 YEVELTEFVSVNGPERIGPHCFELRLVGLGKYGVQVRRVGNLGIYAMKLRK
 AKIVNARDTAFTRARNILTESVVKRPFVLELVAORNGSKLYLECGSGELFPHLE
 REGITLEDCTCYLAETTLAHLGHSOGITTYRDLKPEINIMSSOGHITKLTDPGLCKES
 IHGAVHTFEGCTIEYMAPELIVRSNGHNRADVMSLGLMTDMITLGSPPFAENRKT
 MDKIRGLALRPYLTDPARDLVKKFLKRNPSORIGSGDAADVQRHPRFHNMD
 LLARVDPFPRLOSEEDVQFDTRFRQTPVDSPPDTALSESANQAFLEFTVAPS
 VLDISKEFSRQPKLCSPRRLNSPRAPVSLKFSFGRFSPSLPPTFELPLPPL
 PPPSTTAAPLIRPPSGTKSKSRGRGPR"

BASE COUNT 349 a 538 c 540 g 317 t
 ORIGIN

Alignment Scores:
 Pred. No.: 2,226-132 Length: 1744
 Score: 2572.50 Matches: 489
 Percent Similarity: 99.39% Conservative: 0
 Best Local Similarity: 99.39% Mismatches: 2
 Query Match: 98.41% Indels: 1
 DB: 9 Gaps: 1

US-09-762-258-2 (1-495) x AB019245 (1-1744)

[illegible][illegible]

ORIGIN

Alignment Scores:

Pred. No.: 4,5e-121 Length: 1491
 Score: 2364.50 Matches: 449
 Percent Similarity: 95.05% Conservative: 12
 Best Local Similarity: 92.58% Mismatches: 21
 Query Match: 90.46% Indels: 3
 DB: 10 Gaps: 1

US-09-762-258-2 (1-495) x MMU7938 (1-1491)

QY 14 MetAlaIaIaValAphaeSpleuSpleuGlutThrGluGluGlySerGluGlyGluGlyGlu 33
 Db 1 ATGGCGCGCGGTATTGATTGATTGAGACCGAGAGAGGCGGCGCGCGCGGAA 60
 QY 34 ProGluLeuSerProAlaSpsAlaCysProLeuAlaGluLeuArgAlaIaGlyLeuGlu 53
 Db 61 CCGGAGTTCAGCCCTCGGACGCTGCTCTTGGCGAATTAAAGGCTGCTGGCTGGAG 120
 QY 54 ProValGlyHisArgGluGluValGluLeuThrGluThrSerValAsnValGlyProGlu 73
 Db 121 ACAGTGGACACATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 QY 74 ArgIleGlyProHisCysPheGluLeuLeuArgValLeuGlyGlyGlyGlyGlyGly 93
 Db 181 CCGATCGGGCCCGACGCTTGGAGTACTGAGTACTGGGCGAAGGGGGGCTATGGCAAG 240
 QY 94 ValPheGluValArgThrValGluGlyThrAsnLeuGlyLysIleThrAlaMetLysVal 113
 Db 241 GGTTCACAGTGAAGAAATGGCAGGACCACTTGGGAAATATATGCGATGAAGTTC 300
 QY 114 LeuArgGlyAlaLysIleValArgAsnAlaLysAspThrAlaHisThrArgAlaGluArg 133
 Db 301 TTAAGGAAAGCCCAAGTGTATGACAGTGCAGAGACACAGCCATGCCGGCTGAGAG 360
 QY 134 AsnIleLeuGluSerValLysHisProPheIleValGluLeuAlaThrAlaPheGluThr 153
 Db 361 AACATTCTAGAACTGTGAAAGCATCCCTCATTTGTAAGTGGCTTATGCTCCAGACA 420
 QY 154 GlyGlyLysLeuThrLeuGluGluCysLeuSerGlyGlyLeuPheThrHisLeu 173
 Db 421 GGGGGCAAACTACTACTCATCTCGAGAGTGCCTGAGTGGTGGTGGTCTTCCACACTCT 480
 QY 174 GluArgGluGlyIlePheLeuGluAspThrAlaCysPheThrLeuAlaGluIleThrLeu 193
 Db 481 GAGCGGAAGGAGCATCTTCTCGAAGACACAGCCTGCTTACCTGCACAGATCACACTA 540
 QY 194 AlaLeuGlyHisLeuHisSerGluGlyIleIleThrArgAspLeuLysProGluAsnIle 213
 Db 541 GCCCTGGCCATCTCCATTTCCACGCGCATCATCTACCAGGACCTCAAGCCTGGAACATC 600
 QY 214 MetLeuSerSerGluGlyHisIleLysLeuThrAspPheGlyLeuGlyGlySerIle 233
 Db 601 ATGCTCAGACAGCGGCGGACATCAACATGACAGACTTTGGACTTTGCAAGAGTCCATT 660
 QY 234 HisGluGlyAlaValThrHisThrPheCysGlyThrIleGluThrMetAlaProGluIle 253
 Db 661 CATGAGGAGTCTATCACTACACACTTCTGTGGCACCATGAGTACATGCCCCCAGAGATT 720
 QY 254 LeuValArgSerGlyHisAsnArgAlaValAspThrTrpSerLeuGlyAlaLeuMetThr 273
 Db 721 CTAGTCGGACGTGTACAAACCGGCGAGTGGATGTGGAGCTGGGAGCCCTGAGTCTAC 780
 QY 274 AspMetLeuThrGlySerProProPheThrAlaGluAsnArgLysThrMetAspLys 293
 Db 781 GACATCTCTACGTGATCGCGCCCTTCACTGCGAGAGAACCGGAGAAACTATGATATAA 840
 QY 294 IleIleArgGlyLysLeuAlaLeuProProGlyThrProAspAlaArgAspLeuVal 313
 Db 841 ATCATTAAGGAGAAAGCTGTGTGCGCCCTACCTACCCCGGATGCCGGGAGACTTTGCC 900
 QY 314 LysLysPheLeuLysArgAsnProSerGlnArgIleGlyGlyGlyProGlyAspAlaIa 333

Db 901 AAAAATTCTGAAAGCGGAGACCCCACTAGCAATTGGGGGTGGCTGGGAAATGCTGCT 960
 QY 334 AspValGlnArgHisProPhePheArgHisMetAsnTrpAspSpleuAlaTrpArg 353
 Db 961 GATGTCGAAGGACACCCCTTTTCCGCAATCAATGGAGATGATCTGTGGCCGCGCGC 1020
 QY 354 ValAspProProPheArgProCysLeuGlnSerGluGluAspValSerGlnPheAspThr 373
 Db 1021 GTGAGACCTCCCTTCAGGCGCAAGTGTCAATCAGAAGAGAGATGTGAGCAGTTTGATGCA 1080
 QY 374 ArgPheThrArgGlnThrProValAspSerProAspAspThrAlaLeuSerGluSerAla 393
 Db 1081 CGATTTCACAGCGAGACGCGGTGATGATGATGATGATGATGATGATGATGATGATGAT 1140
 QY 394 AsnGlnAlaPheLeuGlyPheThrTrpValAlaProSerValLeuAspSerIleLysGlu 413
 Db 1141 AACCAAGCCTTCTCGGCTTACATATGAGCACCTTGTCTGAGACGATCAAGAG 1200
 QY 414 GlyPheSerPheGlnProLysLeuArgSerProArgArgLeuAsnSerSerProArgVal 433
 Db 1201 GGCTTCTCTCCAGCGCCCAAGCTGCTCTCCAGACGCGCTTAACAGCAGTCCCGCACCC 1260
 QY 434 ProValSerProLeuLysPheSerProPheGluGlyPheArgProSerProSerLeuPro 453
 Db 1261 CCATAGCGCCCTCAAGTCTCTCCTTGAGGGGTTCGGGCCCACTCCGCGCCACCA 1320
 QY 454 GluProThrGluLeuProLeuProProLeuLeu-----ProProProProProser 470
 Db 1321 GAGCCCATGAGAGCATCTACTCTCAGTCCATACCATCAACACATCAACACACACACACACA 1380
 QY 471 ThrThrAlaProLeuProIleArgProProSerGlyThrLysLysSerLysArgIleArg 490
 Db 1381 AGCAGTGGCCCCCTTCCATCCGCTCCTCCAGAGAACCAAGATCCAAAGAGGAGCGG 1440
 QY 491 GlyArgProGlyArg 495
 Db 1441 GGCCGCTCAGGGCGT 1455
 RESULT 9
 OCG3PK 1778 bp mRNA linear MM 10-JAN-1991
 LOCUS Rabbit mRNA for serine/threonine kinase homologous to ribosomal
 DERIVATION protein S6 kinase.
 ACCESSION X54415
 VERSION X54415.1 GI:1561
 KEYWORDS protein kinase; serine threonine kinase.
 SOURCE Oryctolagus cuniculus.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 REFERENCE 1 (bases 1 to 1778)
 AUTHORS Killmann,M.W.
 TITLE Direct Submission
 JOURNAL Submitted (15-AUG-1990) Killmann M.W., Institut fuer Physiologische
 Chemie, Universitaet Bochum, Postfach 10 21 48, D-4630 Bochum 1,
 FRG
 2 (bases 1 to 1778)
 REFERENCE Hannann,B. and Killmann,M.W.
 AUTHORS cdna encoding a 59 kDa homolog of ribosomal protein S6 kinase from
 TITLE rabbit liver
 JOURNAL FEBS Lett. 273 (1-2), 248-252 (1990)
 MEDLINE 91032193
 PUBMED 1699810
 FEATURES
 source location/Qualifiers
 1..1778
 /organism="Oryctolagus cuniculus"
 /db_xref="taxon:9986"
 /clone="G3"
 <1..1778
 28..1605
 /codon_start=1
 /product="G3 serine/threonine kinase"

```
/protein_id="CAA38279.1"
/db_xref="GI:1562"
/translation="MRRRRRRDGFYPADEPDRRAEDMAGFEDIDIDOPEDAGSEDEL
EGGGLNESMDHGVGVPRYELGMECEKEFEISETVSNKNGPEKIRECEPFLLEVLKGGT
GKRVQVRKVTGANTGKIFAMKVLKAMIVRAKQITAKTRINLEEKHPFIVDLIT
AFQVGRKLYLLELLELLELLELLELLELLELLELLELLELLELLELLELLELLELLE
LKPENIMLNHOGHVKLTDGFLGKESIHGCTVHTFCCGIEYMAELKRSNGRAVDW
WSLGLADMDLTGAPPTGERRKKTIDKILCKNLKPYLLOEARDILKLLKRNAAV
RLGAGPDAGVQAHPPFRHINMEELIARKKPEPKPLDSEEDVSGDSKFTROTPTV
DSPPDSTLSBANOVFLGFTYVASVLESYKESFPEKINSRFRISPTPTSPYK
PSPEDEWKGASASTANDQVPEYPMETSGIEQMDVTTSGEASAPLTPKPNPSPYRK
QAFPMISKREPEHLMNL"
/product="G3 serine/threonine kinase"
mat_peptide
28.1602
/product="G3 serine/threonine kinase"
polya_site
1778
BASE COUNT
555 a 361 c 457 g 405 t
ORIGIN
Alignment Scores:
Pred. No.: 2,51e-87 Length: 1778
Score: 1749.00 Matches: 350
Percent Similarity: 78.17% Conservative: 51
Best Local Similarity: 68.23% Mismatches: 82
Query Match: 66.91% Indels: 30
Gaps: 8
DB: 4
US-09-762-258-2 (1-495) x OCG3PK (1-1778)
QY 1 Metalaarvglyargargalaaarglyalaaala----- 13
Db ATGAGCGACGACGCGGCGGCGCTTTACCGCGCCTGACTCCGACAGCGGAA 87
QY 14 -----Metalaalavalphenspleuspleugluthgluglugsersergluy 30
Db GCTGAGGACATGCTGGAGGTGTTGACATAGACCTGACCCAGACGAGAGCGGCTCT 147
QY 31 Gluglygluproglyleuserprolaaspaalacysproleualaglu---leuarvala 49
Db GAGAGTGAAGCTGGAG-----GAGGGGGCTCAGTTAAATGAAAGCATGGACCAT 195
QY 50 Alaaglyleuglupro-----Valglnhistryglugluvalgluleuthrglu 65
Db GGGGAGATGGGACCATACGAACTTGCAATGAGCAATGAGCAATTTGCAATTCAGAA 255
QY 66 Thrservlaaservlaiglyprogluarqtleglyprohiscysphlegluleuargval 85
Db ACTAGTGTGAACAGAGGCGCAAAAAAATCAGACCAAGATGTTTGAGCTACTTGGGTA 315
QY 86 Leuglylsglygluytyrlylvalphegluvalarglvalaiglnlythraneu 105
Db CTGGTAAAGGGCGCTATGGAAGGTTTTCAGAGTACGGAAGTAAACAGCAAACTACT 375
QY 106 Glyllyslytyrlylvalmetlysalvalarglysalalysilevalargasnaalaysasp 125
Db GGGAAAAAATTTGCTATGAAGGCTTAAAGGCAATGATGTAAGAAATCTAAGAT 435
QY 126 ThrAlaHstThrArgAlaGluArgAsnTleLeuGluSerValLysHisProthelleva 145
Db TTTTCTTCTGACAGAAAGCAAGCAAGCAATATCTCGAGAGAAAGTAAACATCCCTCATTTGG 495
QY 146 GluleuAlaTyraLarPhaGlnThrGlyLysLysLeuTyraLleuGluLysucysSer 165
Db GATTTAATTTATGCTTTCAAGACCGGTGAAACATCTACCTGATCTTGAGATGTCAGT 555
QY 166 GlylgluLuePheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCys 185
Db GGAGGAGAGATTTATTCAGATTGAAGAAGAGGAATATTATGGAAGATACAGCTCC 615
QY 186 PheTyraLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleIetyr 205
Db TTTTACTTGGGAGAAATCTCCATGCTTTGGGCAATTACATCAAAAGGAGATCATCTAC 675
```

```
QY 206 ArgaspLeuLysProGluAsnIleMetLeuSerSerglnGlyHisIleLysLeuthrAsp 225
Db AAGAGACCTGAACCGGAGAAATATCATGCTTAATCAACCAAGGTCATGTAACATACAGAC 735
QY 226 PheGlyLeuCysLysGluSerIleHisGluGlyAlaValThHisIsthPheCysGlyThr 245
Db TTTGACATATGCAAGAAATCCATTCATGATGGAACAGTCACACACACATTTTGGCGAACA 795
QY 246 IleglutyrmAlaProgluIleLeuValaLysSerglyHisAsnArgAlaValAspTrp 265
Db ATGAAATACATGCCCCCTGAAATCTTGATGAGAAGTGGCCACAAATCTGCGCTGATTTGG 855
QY 266 TrpSerLeuGlyAlaLeuMetTyraSpmetLeuthrglySerProPheThrAlaGlu 285
Db TGGAGTTTGGGAGCATTTATATGATGACATGACATGAGAGCAACCCCATTTACTGGGAG 915
QY 286 AsnArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProTyrIleu 305
Db AATAGAAAGAAACAAATGACAAATCCCAATGTAATCAATTTGCTCCCTACCTC 975
QY 306 ThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerglnArgIle 325
Db AACAAGAAAGCCAGAGATGCTTAAAGCTGTAAGAAAGAGCGTCTGCTTACAGTCTT 1035
QY 326 GlylgluLysProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMetAsn 345
Db GGAGCTGCTCCTGGGAGATCTTGAGAGATTCAGAGTCCACCATTTCTTCGACACATTAAT 1095
QY 346 TrpAspAspLeuLeuAlaTrpArgValaAspProPhePheArgProCysLeuGlnSerglu 365
Db TGGGAAAGAACTTCTGATCTGGAAGGAGCGCCCTTAAACCTGTTGCAATCTGAA 1155
QY 366 GluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSerProAsp 385
Db GAGAGTGTAGTCACTTGTATTTCAAGTTTAAACCTGACACACCTGTGTGACAGCCAGAT 1215
QY 386 AspThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTyraValAlaPro 405
Db GACTCAACCTCAGTGAAGTCCCAACGAGCTCTTGAGTTTACATATGCTGCTCA 1275
QY 406 SerValLeuAspSerIleLysGluGlyPheSerPheGlnProLysLeuArgSerProArg 425
Db TCTGTACTTGAAGAGTGAAGAAAGTTTCTTGTGAACCAAAATCCGATCACCTCGA 1335
QY 426 ArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerProPheGlu 444
Db AGATTTATTTGCGACGCCACGAGACCTGTACGCCCAAGTAAATTTCTTGGGATTTTC 1395
QY 445 -----GlyPheArgProSerProSerLeuProGlu---ProThrGluLeuProLeu 460
Db TGGGGAAGAGTGTCTTCAAGCCACGACGCAATTCCTCACACACCTGTGGAATRACCAATG 1455
QY 461 ProProLeuLeuProProProProSerThr-----AlaProLeu 475
Db GAACAAGTGAATGAGACAGATGATGACAGACAAGTGGGGAAGCATCAGCTCCACTT 1515
QY 476 ProIleArgProPro---SerglyThrLysLysSerLys 487
Db CCGATTCGACAGCCGCAACTCCGACCATACAAAAACAA 1554
RESULT 10
AX333655 2346 bp DNA linear PAT 09-JAN-2002
LOCUS AX333655
DEFINITION Sequence 4164 from Patent WO0194629.
ACCESSION AX333655
VERSION AX333655.1 GI:18124374
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
```

Hortigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
gene sets
Patent: WO 0194629-A 4164 13-DEC-2001;
JOURNAL Avallon Pharmaceuticals (US)
FEATURES
source 1. 2346
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 750 a 453 c 558 g 585 t
ORIGIN
Alignment Scores:
Pred. No.: 3,79e-87 Length: 2346
Score: 1748.00 Matches: 354
Percent Similarity: 73.45% Conservative: 50
Best Local Similarity: 64.36% Mismatches: 80
Query Match: 66.87% Indels: 66
DB: Gaps: 8
US-09-762-258-2 (1-495) x AX333655 (1-2346)
QY 1 MetAlaArgLylArgArgAlaArgGlyAlaGlyAlaAla----- 13
Db 28 ATGAGCGGAGCAAGGAGCGGAGCGCTTTTACCAGCCCGGAGCTTCGAGACAGGAA 87
QY 14 -----MetAlaAlaValAPheAspLeuAspLeuGluThrGluGluGlySerGluGly 30
Db 88 GCGAGGACATCGGAGAGGCTTTGACATGACCTGACACGACGACGAGACGCGGCTC 147
QY 31 GluGlyGluProGluLeuSerProAlaAspAlaCysProLeuAlaGlu---LeuArgAla 49
Db 148 GAGGATGAGCTCGAG-----GAGGGGGCTCAGTTAAATGAACATGACCAT 195
QY 50 AlGlyIleuGluPro-----ValGlyHisTyrGluGluGluValGluLeuThrGlu 65
Db 196 GGGGAGATGGACCATGTGAACTTGGCATGAAATCTGTGAATAATTGAAATCTCAGAA 255
QY 66 ThrSerValAsnValGlyProGluArgIleGlyProHisCysPheGluLeuArgVal 85
Db 256 ACATGCTGTAAGAGAGGCGCAGAAAAATACAGACCAATGTTTGTGACACTTCGGGTA 315
QY 86 LeuGlyLysGlyGlyTyrGlyLysValPheGluValArgLysValGlnGlyThrAsnLeu 105
Db 316 CTGGTAAAGGGGCTGTGAAAGCTTTTCAAGTACGAAAGAAAGACAGAGCAAAATACT 375
QY 106 GlyLysIleThrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysAsp 125
Db 376 GGGAAATATTTGCCATGAAAGTGCTTAAAAAGCAATGATAGTAAAGAAATGCTAAAGAT 435
QY 126 ThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPheIleVal 145
Db 436 ACAGCTCATCAAAAGAGAGCAAGAAATATCTGAGAGAAATGAAGCATCCCTTCATCTGTG 495
QY 146 GluLeuAlaTyrAlaPheGlnThrGlyLysLeuTyrLeuIleLeuGluCysLeuSer 165
Db 496 GATTATATTTATGCTTTCAGACTGCGGAAACTCTACCTCACTTGTGATCTCAGT 555
QY 166 GlyGlyLysLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCys 185
Db 556 GAGGAGAACTATTATTTAGCAAAAGAGAGGAATATTATTAAGAGACACAGCTGCG 615
QY 186 PheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleLeuTyr 205
Db 616 TTTTACTTGCAGAAATCTCATGCGCTTTGGGCATTTTACATCAAAAGGGGATCATCTAC 675
QY 206 ArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeuThrAsp 225
Db 676 AGAGACCTGAAGCGGAGAAATATCATCTTAATCACCAGAGTCAATGGAACACTAACAGAC 735
QY 226 PheGlyLysCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThr 245
Db 736 TTGTGACTATGCAAAAGAAATCTATTCATGATGAAACAGTCAACACATCTTTGTGAAACA 795

QY 246 IleGluTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTyr 265
Db 796 ATGAAATACATGGCCCTGAAATCTTGATAGAAAGTGCCACAAATGCTGTGGATTTGG 855
QY 266 TrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThrAlaGlu 285
Db 856 TGGAGTTTGGGACATTTAAATGATGACATCTGACGTGAGACACCCCATTCCTGGGGAG 915
QY 286 AsnArgLysThrMetAlaPlyIleIleArgGlyLysLeuAlaLeuProProTyrLeu 305
Db 916 AATGAAAGAAACAAATGACAAATCTCAAAATGTAACCTCAATTTGCTCCCTTACTTC 975
QY 306 ThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArgIle 335
Db 976 ACACAGAAACCCAGAGATCTGCTTAAAAAGCTCTGAAAAAGAAATGCTGCTTCGCTCG 1035
QY 326 GlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMetAsn 345
Db 1036 GGAAGCTGCTCTGGGAGCGCTGGAGAGTTCAAGCTCATCTCATCTTTAGACACATTAAC 1095
QY 346 TrpAspAspLeuAlaTrpArgValAspProProPheArgProCysLeuGlnSerGlu 365
Db 1096 TGGAGAACTTCTGCTCGAAAGGTGAGCCCTTTAAACCTCTGTTGCAATCTGAA 1155
QY 366 GluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSerProAsp 385
Db 1156 GAGATGTAAGTACAGTTGATTCCAAGTTTACAGCTGACAGACCTGTCGACAGCCAGAT 1215
QY 386 AspThrAlaLeuSerGluSerIleAsnGlnAlaPheLeuGlyPheThrTyrValAlaPro 405
Db 1216 GACTCAACTCTCAGTGAATGTCGCAATCAGCTCTTCTTGGGTTTACATATGTGGTCCA 1275
QY 406 SerValLeuAspSerIleLysGluGlyPheSerPheGlnProLysLeuArgSerProArg 425
Db 1276 TCTGTACTTGAAGCTGGAAGAAAGTTTCTTTTAACCAAAAAATCCATCACTCGA 1335
QY 426 ArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerPro-----Phe 443
Db 1336 AGATTTTGTGACAGCCACAGACACCTGTCAGCCCAATTTTCTCTGGGAGATTTTC 1395
QY 444 GluGlyPheArgProSerProSerLeuProGluProThrGluLeuProLeuProLeu 463
Db 1396 TGGGGAAGAGGTGCTTGGCCAGC-----ACACCAATCTCTCAGACACCTGTG 1443
QY 464 LeuProProProProProSer-----Thr 471
Db 1444 GAATACCAATGCAAAAGTGGCATGACACAGATGATGACATGATGGGAAAGCA 1503
QY 472 ThrAlaProLeuProIleArgProProSerGlyThrLys----- 484
Db 1504 TCGGCACACTTCCAAATAGCAGACGCACTCGGGCCATCAAAAAAAGCTTTTCCC 1563
QY 484 ----- 484
Db 1564 ATGATCTCAAAAGCGCCAGACCACTGCTATGATCTATGACAGACCAATGCTTTTAAT 1623
QY 485 -----LysSerLysArgGlyArgGlyArg 492
Db 1624 GAATTTAAGCAAAAAGGTGAGAGGGAGA 1653
RESULT 11
HUMP70S6KA HUMP70S6KA 2346 bp mRNA linear PRI 27-APR-1993
LOCUS Human p70 ribosomal S6 kinase alpha-I mRNA, complete cds.
DEFINITION
ACCESSION M60724
VERSION M60724.1 GI:189507
KEYWORDS p70 ribosomal S6 kinase alpha-I.
SOURCE Human liver hepatoma, cdna to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2346)

AUTHORS Grove, J.R., Banerjee, P., Balasubramanyam, A., Coffey, P.J.,
 Price, D.J., Avrich, J. and Woodgett, J.R.
 TITLE Cloning and expression of two human p70 S6 kinase polypeptides
 differing only at their amino termini
 JOURNAL Mol. Cell. Biol. 11 (11), 5541-5550 (1991)
 MEDLINE 92017834
 PUBMED 1922062

FEATURES
 source Location/Qualifiers
 1..2346
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_type="hepatoma"
 /tissue_type="liver"
 28..1605
 /codon_start=1
 /product="p70 ribosomal S6 kinase alpha-1"
 /protein_id="AA36410.1"
 /db_xref="GI:189508"
 /translation="MRRRRRDGFYPADEFDRBAEDMAGVFIDLDQPEDAGSEDEL
 EEGQLNEMDHGCVPELGMCEKEFEISETSVNRPEKIRECEPELLVILKGGY
 GKVRQVRKVGANKKIFAMKVLKKAMVRAKRDPAKRNILIEYKHPETIDLY
 AFQSGKLYLLELSGSELMOLERSGIPREDACFTLAISALGHOKGIIIRD
 LKPEINLNHGVHKLDFGLCKESHDGTVHTFCGTEYMAPEILMRSGHNRAVD
 WSLGALVDMLTGAPPTGENRKTIDKILCKLNLPYLTQEARDLKLRNAAS
 RLGAGPDAGEVQAHPEFRHINMELLARKPEPFKPLQSEEDVSOFSKFTQTPV
 FSPDSTLSASANVPLGFTYVAPSVLESVEKESPEKIRSPRFTGSPVSPVK
 FSPGDFWGRGASATANDQPVPEYPMETSGIEQMDVMSGASAPLPIROPNSGRYK
 QAPFMISKREPHLEMLN."

BASE COUNT 750 a 453 c 558 g 585 t

ORIGIN

Alignment Scores:
 Pred. No.: 3,79e-87 Length: 2346
 Score: 1748.00 Matches: 354
 Percent Similarity: 73.45% Conservative: 50
 Best Local Similarity: 64.36% Mismatches: 80
 Query Match: 66.87% Indels: 66
 Gaps: 8

US-09-762-258-2 (1-495) x HUM70S6KA (1-2346)

QY 1 Metalaarqglayargalaaarglvalaglyalaala----- 13
 Db 28 ATGAGGCGACAAAGAGCGCGCTTTTACCACGCCCGACTCCGAGACAGGAA 87
 QY 14 -----MetalaalaValphaspLeuaspLeuGluthrGluGluGluGluGlu 30
 Db 88 GCTGAGGACATGGCGAGAGTGTTCACATAGACCTGGACACGCCAGAGAGCGGCTCT 147
 QY 31 GluGluGluProGluLeuSerProAlaAspAlaCysProLeuAlaGlu---LeuArgAla 49
 Db 148 GAGATGAGCTGGAG-----GAGGGGGCTCAGTTAAATGAAGACATGGACCAT 195
 QY 50 AlaGlyLeuGluPro-----ValGlyHisTyrGluGluValGluLeuThrGlu 65
 Db 196 GGGGAGTGGGACCATATGAACCTTGGCAATGTGTGAGAAATTTGAATCTCAGAA 255
 QY 66 ThrSerValaasnValGlyProGluArgTlleGlyProHisCysPheGluLeuLeuArgVal 85
 Db 256 ACTAGTGGAAACAGAGGCGCGAAATAATACAGACGAATGTTTGGCTACTTGGGTA 315
 QY 86 LeuGlyLysGlyLysTyrGlyValPheGluValArgLysValGlnGlyThrAsnLeu 105
 Db 316 CTGGTAAGGGGGCTATGGAAGGTTTTCAGATACGAAAGATACAGAGACCAATACT 375
 QY 106 GlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysAsp 125
 Db 376 GGGAAATAATTTGGCCATGAAGGCTTAAAGGCAATGATGTAAGAAATCTAAGAT 435
 QY 126 ThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProHelleVal 145
 Db 436 ACAGCTCATACAAAGACAGACGAATTTCTGGAGGAAAGTAAAGCATCCCTTCATCGTG 495

QY 146 GluLeuAlaTyrAlaPheGlnThrGluGlyLysLeuTyrLeuIleLeuGluCysLeuSer 165
 Db 496 GATTTAATTTATGCGCTTTCAGACTGGTGAATAACTCTACCTCATCTGATATGTCAGT 555
 QY 166 GlyIleGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCys 185
 Db 556 GGAGGAGAACTATTATATGCGATGTAAGAGGAGGAATATTATGGAACACACTGCTTC 615
 QY 186 PheTyrLeuAlaGluIlePheThrLeuAlaLeuGluHisLeuHisSerGlnGlyIleLeuTyr 205
 Db 616 TTTTACTTGGCAGAAATCTCCATGGCTTGGGCGATTTATCATCAAAAGGGGATCATCTAC 675
 QY 206 ArgAspLeuLysProGluLysAsnIleMetLeuSerSerGlnGlnHisIleLysLeuThrAsp 225
 Db 676 ACAGACCTGACACCCGAGAGATATCATGCTTATACACAAAGGTCATGTGAACATACAGAC 735
 QY 226 PheGlyLeuCysLysGluSerIleHisGluIleValAlaValThrHisThrPheCysGlyThr 245
 Db 736 TTTGACACTGCAAGAAATCTATTTCATGATGGAAACAGTCACACACATTTTGTGGAAACA 795
 QY 246 IlegIuTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTyr 265
 Db 796 ATAGAAATACATGCCCCCTGAATCTTGATGAAGAAGGCCACAAATCTGCTGGATTTGG 855
 QY 266 TrpSerLeuGlyAlaLeuMetLysAspMetLeuThrGlySerProProPheThrAlaGlu 285
 Db 856 TGGAGTTTGGAGCATTAATATGATGACATGCTGACATGGAGACCCCATTCCTGGGAG 915
 QY 286 AsnArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProTyrLeu 305
 Db 916 AATAGAAAGAAACAATGATACAAATCTCAATGTAATCAATTTGCTCCCTACCTC 975
 QY 306 ThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArgIle 325
 Db 976 ACACAAGAACCCAGAGATGCTGCTTAAAGAGCTGTAAGAAAGAAAGCTGCTGCTGG 1035
 QY 326 GlyGlyLysProGlyAspAlaAlaAspValGlnArgHisProPheArgHisMetAsn 345
 Db 1036 GGAGCTGTCCTGGGGAGCCCTGGAGAGATTCAGATCCATCTTTTATGACATTTAAC 1095
 QY 346 TrpAspAspLeuLeuAlaTrpArgValAspProProPheArgProCysLeuGlnSerGlu 365
 Db 1096 TGGGAAGAACTTCTGCTGTCGAAGGTGAGAGCCCTTTAAACCTCTGTCGAATCTGAA 1155
 QY 366 GluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSerProAsp 385
 Db 1156 GAGATGTAGTCAAGTTGATTCAAAGTTTACACGTCAGACACCTGTGCACAGCCAGAT 1215
 QY 386 AspThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTyrValAlaPro 405
 Db 1216 GACTCAACTCTCAGTGAAGAGTCCAAATCGATCGTCTTCTGGTTTATCATATGGCTCCA 1275
 QY 406 SerValLeuAspSerIleLysGluGlyPheSerPheGlnProLysLeuArgSerProArg 425
 Db 1276 TCTGTACTTGAAGAGTGTGAAGAAAGTTTCTTGTGAACCAAAATCCGATCACCTCGA 1335
 QY 426 ArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerPro-----Phe 443
 Db 1336 ACATTTATTGGCAGCCACGAGAACCTGTCAACCGCATGTAATTTTCTCTGGGATTTTC 1395
 QY 444 GluGlyPheArgProSerProSerLeuProGluProThrGluLeuProLeuProLeu 463
 Db 1396 TGGGGAAGAGTGCTTGGCCACG-----ACAGCAAAATCCTGACAGACCTGTG 1443
 QY 464 LeuProProProProProSer-----Thr 471
 Db 1444 GAATACCCCAATGAACAAGTGGCATAGACAGATGATGTGACATGAGTGGGAAGACA 1503
 QY 472 ThrAlaProLeuProIleArgProProSerGlyThrHis----- 484
 Db 1504 TCGGACACCTTCCATATGACAGCCGGAAGCTGTGGGCCATACAAAAACAAGCTTTTCC 1563
 QY 484 ----- 484

Db 1564 ATGATCTCCAAAGCGCAGACGACCTGCGTATGATCTATGACAGCAATGCTTTAAT 1623
Qy 485 -----LysSerLySArgLyArgLyArg 492
Db 1624 GATTTAAGCAAAAGGTGGAGAGAGAG 1653

RESULT 12
RATS6KIN3
LOCUS RATS6KIN3 1800 bp mRNA linear ROD 27-APR-1993
DEFINITION Rat S6 kinase mRNA, complete cds.
ACCESSION M57428 M35864
VERSION M57428.1 GI:206839
KEYWORDS S6 kinase.
SOURCE Rat (Sprague-Dawley) liver, cDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1800)
AUTHORS Kozma,S.C., Ferraril,S., Basand,P., Siegmann,M., Totty,N. and Thomas,G.
TITLE Cloning of the mitogen-activated S6 kinase from rat liver reveals an enzyme of the second messenger subfamily
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (19), 7365-7369 (1990)
MEDLINE 91017506
PUBMED 1699226

REFERENCE 2 (sites)
AUTHORS Lane,H.A., Morley,S.J., Doree,M., Kozma,S.C. and Thomas,G.
TITLE Identification and early activation of a Xenopus laevis p70s6k following progesterone-induced meiotic maturation
JOURNAL EMBO J. 11 (5), 1743-1749 (1992)
MEDLINE 92258384
PUBMED 1374712

FEATURES
source location/Qualifiers
1..1800 /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="liver"
/dev_stage="7-8 week"
/tissue_11b="stratagene lambda zap II 936507"
1..1800 /gene="S6 kinase"
134..1642 /gene="S6 kinase"
/codon_start=-1
/product="S6 kinase"
/protein_id="AAA42103.1"
/db_xref="GI:206840"
/translation="MAGVFDIDLPQEDAGSDELEEGGQLNESMDHGCGVPELME
HCEKEISETSVNRGPEKIRPECFELRYLKGKGVQVRRKVTGAMGKLEAMVL
KKAMIVRNKQFANHKAERNILIEVKNHPYIDLIYAFOFGSKLILELISGSELMO
LEREGTMEWDCPYLAETISMLGHLHOGCITLRDKPENIMLNHGHKYLDRGICK
ESTIHGTVHTTCGTEIYMAPELIMSGHNRAVDWMSLGADGAEVQNHPEFRITNM
KITDKILKCLNLPYLYQEARDLKLLKRNAAASKLGPEDAGVQNHPEFRITNM
EDLARKEPPEPKPLIOSEEDVSQDSKRTQTPVDSPPDSPLSEANOVFGFTYVA
PSVLSVKEKFESEFKIRSPRFISGTPSPVPSFDFGMRGASASTAMPQRPVE
YPMETSGIOMDVTTSGEASADLPTRPPNSGPKKQAFMISKRPHELMN."

BASE COUNT 556 a 355 c 464 g 425 t
ORIGIN

Alignment Scores:
Pred. No.: 3..71e-87 Length: 1800
Score: 1746.00 Matches: 344
Percent Similarity: 80.618 Conservative: 51
Best Local Similarity: 70.208 Mismatches: 75
Query Match: 66.794 Indels: 20
DB: 10 Gaps: 7

US-09-762-258-2 (1-495) x RATS6KIN3 (1-1800)
Qy 14 MetAlaAlaValAlaPheAspLeuAspLeuGluThrGluGluGlySerGluGluGlyGlu 33

Db 134 ATGGCAGAGAGTGTATTGACATAGACCTGGACCCAGACAGAGANTCAGGCTCTGGATGAG 193
Qy 34 ProGluLeuSerProAlaAspValCysProLeuAlaGluLysLeuArgAlaAlaGlyLeu 52
Db 194 CTGGAG-----GAGGGGGTCACTTAATGAAGCATGGACCATGGGGAGTT 241
Qy 53 GluPro-----ValGlyHisTyrGluGluValGluLeuThrGluThrSerVal 68
Db 242 GGACCATATGAACTGGCATGCAACATGTGGAAATTTGAATTCACGAATCTAGTGTGTC 301
Qy 69 AsnValGlyProGluArgGlyLeuGlyProHisCysPheGluLeuLeuArgValLeuGlyLys 88
Db 302 AACAGAGGGCCAGAAAAAACAAGACAGCAATGTTTGAGCTACTTGGGACTTGGTAA 361
Qy 89 GLYGLTYTyrGlyLysValPheGluValArgLysValGlnGlyThrAsnLeuGlyLysIle 108
Db 362 GGGGGCTATGGAAAGGTTTTTCAAGTACGAAAGTAAAGCAAGCAAAATCTGGGAAGAT 421
Qy 109 TyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysAspThrAlaHis 128
Db 422 TTGGCCATGAAGGTGCTTAAGAGCAATGATGTAAGAAATGCTAAAGATACAGCTCAT 481
Qy 129 ThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPheIleValGluLeuAla 148
Db 482 ACAAAAGCAGAGGGAATATTCGAGGAAGTAAACATCCCTTCATCGTGATTTAAAT 541
Qy 149 TyrAlaPheGlnThrGluGlyLysLeuTyrLeuIleLeuGluCysLeuSerGlyGlyGlu 168
Db 542 TATGCTTTCAAGCCGGTGGAAACCTCTACCTGATCTTCACTCACTGAGAGAGAA 601
Qy 169 LeuPheThrHisLeuGluArgGlyLysIlePheLeuGluAspThrAlaCysPheTyrLeu 188
Db 602 CTATTATGCAATTAAGAAAGAGAGGAGATTCATGTAAGATACAGCTGCTTTACTTG 661
Qy 189 AlaGluIleThrLeuAlaLeuGlyLysLeuHisSerGlnGlyIleTyrArgAspLeu 208
Db 662 GCGAAATCCCATGCTGGGCGCATTTAATCAATCAAAAGGATCATCTACAGACGCTG 721
Qy 209 LysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeuThrAspPheGlyLeu 228
Db 722 AACCCGAGAACATCATGCTTAAATACCAAGGTCAGGTGAGAGTGCACACTTTGGACAT 781
Qy 229 CysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThrIleGluTyr 248
Db 782 TGCAAGAAATCTATGATGATGAGAACAGTCCACACATATTTGTGGAACAATAAGATAC 841
Qy 249 MetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTyrTrpSerLeu 268
Db 842 ATGGCCCTGAAATCTTGATGAGAACGCGCCACACCCGTCGTGATGCTGGAGCTTGG 901
Qy 269 GlyAlaLeuMetTyrAspMetLeuThrGlySerProPheThrAlaGluAsnArgLys 288
Db 902 GGAGCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 961
Qy 289 LysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProGlyLeuThrProAsp 308
Db 962 AAAACAATTAACAATAATCCCAATGTAATTAATTTGCTCCCTACCTCACACAAGAA 1021
Qy 309 AlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArgIleGlyGly 328
Db 1022 GCTCGAGATCTGCTTAAAAAGCTGCTGAAAAGAAAGTCTGCTGCTGCTGAGCTGGC 1081
Qy 329 ProGluLysAlaAlaAspValGlnArgHisProPhePheArgHisMetAsnTrpAsp 348
Db 1082 CCTGGGAGTCTGGAGAAAGTCCAAAGCGCATCTTTTATGACACATTAATCTGGAAAG 1141
Qy 349 LeuLeuAlaTrpArgValAspProPheArgTrpCysLeuGlnSerGluAspVal 368
Db 1142 CTTTGGCTCGAAGGAGGAGCCCTTTAAGCTCTGTGCAATCTGAAGAGATGAG 1201
Qy 369 SerGluPheAspThrArgPheThrArgGluThrProValAspSerProAspAspThrAla 388

Db 1202 AGCAGTTGGATTCAAGTTTACTGCTGACACCTGTTGACGCCCGATGATCTCACT 1261
OY LeuSerGIuSerAlaAsnGlnAlaPheLeuGlyPheThrTyValAlaProSerValIleu 408
Db 1262 CTCAGTGAAGAGTCCACACAGGCTCTTCTGGGTTTACTATGAGCTCAGCTGACT 1321
OY AspSerIleuGlyGlyPheSerPheGlnProLysIleuArgSerProArgIleuAsn 428
Db 1322 GAAAGTGAAGAAAGAGTTTCTTTTGACCAAAAATCCGATCCGCTGAGAGATTAT 1381
OY 429 SerSerProArgValProValSerProLeuLysPheSerProPheGlu----- 444
Db 1382 GGTACCCACGAAACCGCTGTCAGCCAGTCAATCTCTCTGCGGAGATTCTGCGGACGA 1441
OY 445 GlyPheArgProSerProSerIleuProGlu---ProThrGluLeuProIleuProIleu 463
Db 1442 GGTGCTTACGCCACGACGACCAATCTCTGACACACCTGTGGAATACCAATGGAACAACT 1501
OY 464 LeuProProArgProProSerThrThr-----AlaProIleuProIleuArg 478
Db 1502 GGAATAGAGACAGATGATGTGACAAAGCGGGGGAAGCTTTCAGCGCACTTCCAAATCCGA 1561
OY 479 ProPro-----SerGlyThrLysLysSerLys 487
Db 1562 CAGCCCAACTCTGGCCATACAAAAACAA 1591

RESULT 13

HUMP70S6KB

LOCUS HUMP70S6KB 1791 bp mRNA linear PRI 27-APR-1993
DEFINITION Human p70 ribosomal S6 kinase alpha-II mRNA, complete cds.
ACCESSION M60725.1 GI:189509
VERSION p70 ribosomal S6 kinase alpha-II.
KEYWORDS Human liver hepatoma, cDNA to mRNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Grove, J.R., Banerjee, P., Balasubramanyam, A., Coffey, P.J.,
Price, D.J., Avruch, J. and Woodgett, J.R.
TITLE Cloning and expression of two human p70 S6 kinase polypeptides
differing only at their amino termini
JOURNAL Mol. Cell. Biol. 11 (11), 5541-5550 (1991)
MEDLINE 92017834
PUBMED 1922062

FEATURES

Source location/Qualifiers
1..1791 /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="hepatoma"
/tissue_type="liver"
99..1607 /codon_start=1
/product="p70 ribosomal S6 kinase alpha-II"
/protein_id="AAA36411.1"
/db_xref="gi:189510"
translation="MAGVFDDIDDPEDAGSEDELEEGGLNESMDHGQVPELQME
HCEKEISETSVNGRQPEKIRRECELLRLVKKGCGKQVQURKATGATGKTPKAKVL
KKATVRRAKTATTKAKRNILEEKHPFIVDLIYAFGTGRLLILEYLSGDELQ
LERGIFMEDPACFYLAETISALGLHKGILIRDLKENTGLNHNQGVKLTGDELK
ESHDGTITFECCSTIEYMAPEILMRSGHNRAVDWMSGALMYDMLTGAPPTGENK
KTIDILKCLNLPYLTQEARDLKTLKNNASRLGAGGDADEVGAHPFTGINN
ELLARKVEPFPKLLQSEEDVSQFDSFTTQTFOTVSDSDSTLSSANOVRLGFTYVA
PSYLSVKEKSFEPKIRSPRRIGSPPTSPKPSFGSDWGRASASTAMPQIPE
YPMETSGIEQMDVMSGEASAPLPTRQNSGPYKQAPMLSKREHLRMN."

CDS

BASE COUNT 585 a 354 c 438 g 414 t
ORIGIN

Alignment Scores:

Pred. No.: 4.18e-87 Length: 1791
Score: 1745.00 Matches: 348
Percent Similarity: 75.52% Conservative: 50
Best Local Similarity: 66.03% Mismatches: 73

Query Match: 66.76% Indels: 56
DB: 9 Gaps: 7
US-09-762-258-2 (1-495) x HUMP70S6KB (1-1791)
OY 14 MetaIaIaValaPheAspLeuAspLeuGlnIleuGlySerGluGlyGlu 33
Db 99 ATGGCAGGAGTGTGTTGACATGACCTGGACGACGACGAGGAGGCGCTGTGAGGATGAG 158
OY 34 ProGluLeuSerProAlaAspAlaCysProIleuAlaGlu---LeuArgAlaIleGlyLeu 52
Db 159 CTGGAG-----GAGGGGGTCAATTAATGAAGCATGAGCATTGAGGAGAGT 206
OY 53 GluPro-----ValGlnHisTyrgluGluValaGluLeuThrSerVal 68
Db 207 GGACCATATGAACCTTGCGCATGGAACATTGTGGAATTTGAAATCTCAGAAATCTAGTGTG 266
OY 69 AsnValGlyProGluArgIleGlyProHisCysPheGluLeuArgValLeuGlyLys 88
Db 267 AACAGAGGCGCAGAAAAAATCAGACCAGAAATGTTTGACCTACTTGCGGTGTA 326
OY 89 GlyGlyTyrglyLysValPheGlnValArgLysValGlnGlyThrAsnLeuGlyLysIle 108
Db 327 GGGGGCTATGGAAGGTTTTCAGAGTACGAAAAAGTAACAGAGCAATATCTGGAAAAATA 386
OY 109 TyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysPthrAlaHis 128
Db 387 TTTCGATATGAGTGTCTTAAAGGCAATGATGATGAAATGCTAAATATCAGCTCAT 446
OY 129 ThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPheIleValGluLeuAla 148
Db 447 ACMAAAGCAGAAACGGAATATCTGGAGGAATGAAGCATCCCTTCATCTGTGATTAAAT 506
OY 149 TyrAlaPheGlnThrGlyLysLysLeuTyrlleuGluCysLeuSerGlyGlyGlu 168
Db 507 TATGGCTTTCACAGCTGGTGGAAAACTTCATCTGATATCTCATGCTGAGAGAGAA 566
OY 169 LeuPheThrHisLeuGluArgGlyLysIlePheLeuGluAspThrAlaCysPheTyrlleu 188
Db 567 CATTTATGACACTGTAGAAAGACGGAATATTATGGAAGACACAGCTGCTTTTACTTG 626
OY 189 AlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleIleTyrgArgAspLeu 208
Db 627 GCAGAAATCTCATGCTGCTTGGGCGATTATCAACAAAGGAGATCATCTACAGACACCTG 686
OY 209 LysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeuThrAspPheGlyLeu 228
Db 687 AAGCCGGAAGATATCATGCTTATATCACCAAGGTCATGTAACCTAACACACTTTGGACTA 746
OY 229 CysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThrIleGlyTyrl 248
Db 747 TGCMAAGATCTATTCATGATGGAACAGTCACACACACATTTTGTGGAACATATGATATC 806
OY 249 MetaIaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTrpTrpSerLeu 268
Db 807 ATGGCCCCGGAATCTGTATGAGAGTGGCCCAACATCGTGTGATGGAGACTTGG 866
OY 269 GlyAlaLeuMetCysTyrlAspMetLeuThrGlySerProProPheThrAlaGluAsnArgLys 288
Db 867 GGAGCATTAATATGATGACATGCTGACTGAGGACACCCCACTTCACTGGGAGATAGAAAG 926
OY 289 LysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProProTyrlleuThrProAsp 308
Db 927 AAAACATATGACAAATCTCAAAATGTAACTCAATTTCTCCCTCACTCAACACAGAA 986
OY 309 AlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArgIleGlyGly 328
Db 987 GCCAGAGATCTGCTTAAAAAGCTGCGTGAAGAAATATGCTTCCTGCTGGAGCTGCT 1046
OY 329 ProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMetLsnTrpAsp 348
Db 1047 CCTGGGAGACGTGAGAAAGTCAAGCTCATTCATCTTATGACACATTAATCTGGGAAGAA 1106

QY 349 LeuLeuAlaTrpArgValAspProProPheArgProCysLeuGlnSerGluGluAspVal 368
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1107 CTCTCGTGCAGAAAGGGAGGCCCTTTAAACCTCTTGCAATCTGAAGAGATGTA 1166
QY 369 SerGlnPheAspThrArgPheThrArgGlnThrProValAspSerProAspAspThrAla 388
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1167 AGTCAGTTGATTCACAAAGTTTACAGCGACACCTGTCAGACGCCAGATGACTCAACT 1226
QY 389 LeuSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTyValAlaProSerValLeu 408
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1227 CTCAGTGAAGTGCATACGATCGCTTCTTGCGTTTACATATGGCTCATCTGACTT 1286
QY 409 AspSerTleuGluGluPheSerPheGlnProLysLeuArgSerProArgArgLeuAsn 428
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1287 GAAAGTGTGAAGAAAGAAAGTTTCTTCTTGAACCAAAATCCGATCACCCTGAGATTATTT 1346
QY 429 SerSerProArgValProValSerProLeuLysPheSerPro-----PheGluGlyPhe 446
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1347 GGCAGCCCAAGAACCTGTCAGCCCAAGTCAAAATTTCTCTGCGGATTTCTGGGGAAGA 1406
QY 447 ArgProSerProSerLeuProGluProThrGluLeuProLeuProProLeuLeuProPro 466
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1407 GGGCTTCGGCCAGC-----ACAGCAATCTCAGACACCTGTGGAAATACCA 1454
QY 467 ProProProSer-----ThrThrAlaPro 474
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1455 ATGAAACAAGTGGCATAGACAGATGATGTGACATGATGGGAAAGCATCGGCACCA 1514
QY 475 LeuProTleArgProProSerArgLys----- 484
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1515 CTTCACATACGACAGCGCAACTCTGGGCCATACAAAAACAAGCTTTCCCATGATCTCC 1574
QY 485 -----Lys 485
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1575 AAAGGCCAGAGCACTGCTATGATCTATGACAGCAATGCTTTTAATGAATTTAAG 1634
QY 486 SerLysArgGlyArgGlyArg 492
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1635 GCAAAAGGTGAGAGGAGA 1655
RESULT 14
RAT56PK 2287 bp mRNA linear ROD 27-APR-1993
LOCUS 2287 bp mRNA linear ROD 27-APR-1993
DEFINITION Rat S6 protein kinase mRNA, complete cds.
ACCESSION M58340.1 GI:206841
VERSION M58340.1 GI:206841
KEYWORDS S6 protein kinase; Insulin/mitogen stimulated protein kinase; p70
SOURCE Rat, cDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2287)
AUTHORS Banerjee,P., Ahmed,M.F., Grove,J.R., Kozlosky,C., Price,D.J. and
Avruch,J.
TITLE Molecular structure of a major insulin/mitogen-activated 70-kDa S6
protein kinase
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (21), 8550-8554 (1990)
MEDLINE 91046033
PUBMED 2236064
FEATURES
source location/Qualifiers
1..2287
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/cell_line="hepatoma line H4IIEC3"
/cistone_11b="Iambda gtl1 PB4"
22..1599
/codon_start=1
/product="S6 protein kinase"
/protein_id="AAA42104.1"
/db_xref="GI:206843"
/translation="MRRRRRDSGFYPADFRHREADMAGVFDIDLDQPEBDSDEEL

EEGGQINESMDHGVPYELGMEHCEKEIEISTSVNRGPEKTRPECFELLRYLKGCGY
GVFQVRKVTGANTGKIFAMKVLKRAMIYRANKDVAHTAEKNILEEKNHPITVLILY
AFOTGGKLTLEILEYSGEGLFQLEBEDTGFEMEDTACFYLAETSMALGHIHQKILYRD
LKPENIMNHQHVKLTDGELCKESIHODTFTHTPGCTEYAWAPELTMGSNNRAVD
WSIGALMDMLTGAPPEGNEKKRTIDTLCKIKLNPPLYTOEADLIDKLKLRNAAS
RIGACGPDAGEYQAHFPPRHIMBELIARKVRPRPKPLIOSEDDYSDPSKTRQTPV
DSBDSSTLESANOVFLGPTVYAPSVLESVKKFSPEKTRSPRIRISPRIPVSVK
FSPDFWGRGASASTANPQTPVEYPMETSIGIDMDVTSIGEASAPLPIRPNSGPYKK
QAFPMISKRPEHLRMNL"
BASE COUNT 733 a 446 c 540 g 568 t
ORIGIN
Alignment Scores:
Pred. No.: 1,01e-86 Length: 2287
Score: 1740.00 Matches: 349
Percent Similarity: 77.97% Conservative: 51
Best Local Similarity: 68.03% Mismatches: 83
Query Match: 66,568 Indels: 30
DB: 10 Gaps: 8
US-09-762-258-2 (1-495) x RAT56PK (1-2287)
QY 1 MetAlaArgLysArgAlaArgValAlaGlyAlaAla----- 13
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 22 ATGAGCGCAGACGAGGCGGAGCGCTTTTACCACGCGCTGACTTCGACACAGGAA 81
QY 14 -----MetAlaAlaValPheAspLeuAspLeuGlnThrGluGluSerGluGly 30
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 82 GCTGAGGACATGGCAGGAGGCTTTGACATGACCTGGACACGACGACGATGAGGCTCT 141
QY 31 GluGlyGluProGluLeuSerProAlaAspAlaCysProLeuAlaGlu---LeuAlaGly 49
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 142 GAGGATGAGCTGGAG-----GAGGGGGGTGCTGTTAATGAAACATGGACCAT 189
QY 50 AlAGlyLeuGluPro-----ValGlyHisTyrgLysValGluLeuThrGlu 65
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 190 GGGGAGTGTGACCATATGACTTGGCATGGAACATTTGTGAAATTTGAAATCTCGAA 249
QY 66 ThrSerValAsnValGlyProGluArgLysGlyProHisCysPheGluLeuArgVal 85
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 250 ACTAGTGTGAACAGAGGCGGCAAAAAATCAGACAGCAAGATGTTTGAGCTACTCGGTA 309
QY 86 LeuGlyLysGlyGlyTyrgLysValPheGlnValArgLysValGlnGlyThrAsnLeu 105
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 310 CTGGTAAAGGGGCTATGAAAGGTTTTCAGATGAGAAAGTAACAGGACGAAATACT 369
QY 106 GlyLysLysThrAlaMetLysValLeuArgLysAlaLysTleValArgAsnAlaLysAsp 125
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 370 GGGAGATATTGGCATGAAAGGTGCTTAAAGGCAATGATAGCAATGCTAAAGAT 429
QY 126 ThrAlaHisThrArgAlaGluArgAsnTleLeuGluSerValLysHisPropheIleVal 145
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 430 ACAGCTCATCAAAAGACAGAGCGGAATATCTCGAGGAATAAAGCATCCCTCATTTGT 489
QY 146 GluLeuAlaTyrrAlaPheGlnThrGlyGlyLysLeuTyrrTleuTleuGluCysLeuSer 165
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 490 GATTTAATTTATGCTTTCAGACCGGTGAAACTCTACCTCACTCTTGAGTATCTCAGT 549
QY 166 GlyLysLysLeuPheThrHisLysGluArgGlyLysTlePheLeuGluAspThrAlaCys 185
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 550 GAGAGAGACATATTATGACGACTTAGAAAGAGAGGCAATATTCATGGAAGATACAGCTTC 609
QY 186 PheTyrrLeuAlaGluTleThrLeuAlaLeuGlyHisLysHisSerGlnGlyTleTyrr 205
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 610 TTTTACTTGCTGCAAAATCTCCATGAGCTTTGGGCAATTATCATCAAAAGGATTAATCTAC 669
QY 206 ArgAspLeuLysProGluAsnTleMetLeuSerSerGlnGlyHisTleLysLeuThrAsp 225
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 670 AGAGACCTGAAGCGGGAACATCATGCTTAATCACCAGAGTACGGAAGCTGACAGAC 729
QY 226 PheGlyLeuLysLysGluSerTleHisGlyAlaValThrHisThrPheCysGlyThr 245
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 730 TTGGACTATGCAAGACATCTATTCTATGATGAAACAGTCAAGACACATTTTGTGGACAA 789

QY 246 ILeGlyTyrMetAlaProGluIleuValArgSerGlyHisAsnArgAlaValAspTyr 265
 DB 790 ATAAATATCATGCGCCCTGGAATCTTGATGAGAAAGCGCCCAACCGCTGCTGATGG 849
 QY 266 TTrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThrAlaGlu 285
 DB 850 TGGAGCTGGAGCATTAATGATGACATGCTGACTGGAGCACTCCATTCACCTGGGAG 909
 QY 286 AsnArgLysTyrThrMetAspLysIleLeuArgGlyLysLeuAlaLeuProTyrLeu 305
 DB 910 AATGAAAGAGCAATGACAAAATCTCAAAATGTAATTAATTTGCCCTCCTACTC 969
 QY 306 ThrProAspAlaArgAspLeuValLysLysPheLeuValArgAsnProSerGlnArgTle 325
 DB 970 ACACAAAGACGTCAGATCTCTTAAAAAGCTGTGAAGAGAAATGCTGCTTCGCTCTT 1029
 QY 326 GlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMetAsn 345
 DB 1030 GGACCTGGCCCTGGAGTGTGGAGAGTCCAGCGCATTCATTTTATAGACATTAAC 1089
 QY 346 TTrpAspSerLeuLeuAlaTTrpArgValAspProPheArgProGlySerGlu 365
 DB 1090 TGGGAAAGCTTTTGGCTGGAGAGTGGAGCGCCCTTTAAGCCTCTGTTCAATCTGAA 1149
 QY 366 GluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSerProAsp 385
 DB 1150 GAGATGTGAGTCAGTGTGATTCAAAGTTTACTGTCAGACACCTGTTGACACGCCCAT 1209
 QY 386 AspThrAlaLeuSerGlnSerAlaAsnGlnAlaPheLeuGlyPheThrTyrValAlaPro 405
 DB 1210 GACTCACTCTCAGTGAAGAGCCACACGCTCTTGGGTTTACATATGTGGCTCA 1269
 QY 406 SerAlaLeuAspSerIleLysGlyLysPheSerPheGlnProLysLeuArgSerProArg 425
 DB 1270 TCTGTACTTGAAGTGTGAAGAAAGTTTCTTTTGAACCAAAAATCCGATCCCTCGA 1329
 QY 426 ArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerProPheGlu 444
 DB 1330 AGATTATTGTGTAGCCACGACGACGCTGTCAGCCAGCAATCTCTCTCGGGGATTTTC 1389
 QY 445 -----GlyPheArgProSerProSerLeuProGlu---ProThrGluLeuProLeu 460
 DB 1390 TGGGAGGAGGTGCTTACAGCAGCAGACAGCAATCTCAGACACCTGTGGATACCCATG 1449
 QY 461 ProProLeuLeuProProProProSerThrThr-----AlaProLeu 475
 DB 1450 GAAACAAAGTGGAATAGACAGATGATGTGACAAAGCGGGGAAAGCTTCAGCGCCACTT 1509
 QY 476 ProIleArgProPro-----SerGlyThrLysLysSerLys 487
 DB 1510 CCAATCCGACAGCCCAACTCTGGGCCATACAAAACAA 1548
 RESULT 15
 XLA131521 1717 bp mRNA linear VRT 30-MAR-1999
 LOCUS Xenopus laevis mRNA for p70 S6 kinase.
 DEFINITION A1131521
 ACCESSION A1131521 GI:4582254
 VERSION A1131521.1
 KEYWORDS kinase; s6k1 gene.
 SOURCE Xenopus laevis.
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 Xenopodinae; Xenopus.
 REFERENCE 1 (bases 1 to 1717)
 AUTHORS Schwab,M.S., Kim,S.H., Terada,N., Edfjall,C., Kozma,S.C., Thomas,G.
 and Maller,J.L.
 TITLE p70(S6K) controls selective mRNA translation during oocyte
 maturation and early embryogenesis in Xenopus laevis
 JOURNAL Mol. Cell. Biol. 19 (4), 2485-2494 (1999)
 MEDLINE 99182435
 PUBMED 10082514

REFERENCE 2 (bases 1 to 1717)
 AUTHORS Kozma,S.C.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-1998) Kozma S.C., Growth Control, Friedrich
 Miescher Institute, P.O. Box 2543 Basel, CH-4002, SWITZERLAND
 FEATURES
 source location/Qualifiers
 1..1717
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 gene /db_xref="GI:4582255"
 /db_xref="s6k1"
 /gene="s6k1"
 /codon_start=1
 /product="kinase"
 /protein_id="CAB40193.1"
 /translation="MAGVFDIDIDDPEDATISDDELDEGTFIEPMHGSIYEIGMEH
 CEFKEISEISVNGKPEKIRECEFEELVLKGGYGVYKRYVGAHTGKIFPKVLYK
 KAMIVRAKDTAHRKARNITLSEYKHPFDLYAFQGTGKLYLIEYLSGGELFMOL
 ERGIEPEPRACEYLAIESMALGHLOKGIITYDLPKREINMLNIGYKLTDEGLCKE
 SHDGTHTFCGCTIETWAPETILKRSNHNRAVDWMSLGALMTDLTGAPFSGENRK
 TIDKLCKNLNLPYLTQEARDLTKLKRNAASRLGAGVDGVDVGGSHFPHIIMD
 DLARKEPPEPKFLOSIEDVSOFSKFTQTPVDSPDDATLSEANOVGFETVAP
 SYLESVEKFSFEPKIRSPRFTSPVPVSPKFSADIMARCTAGTNTQTPGPF
 RMEAGGVEMDVTYSGEASAPLPIROSNAQPKYKQAYPIISKREHRLMNL"
 BASE COUNT 521 a 342 c 418 g 436 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,98e-84 Length: 1717
 Score: 1692.50 Matches: 337
 Percent Similarity: 76.65% Conservative: 47
 Best Local Similarity: 67.27% Mismatches: 72
 Query Match: 64.75% Indels: 45
 DB: Gaps: 7
 US-09-762-258-2 (1-495) x XLA131521 (1-1717)
 QY 8 ArgGlyAlaGly-----AlaAlaMetAlaAlaValPheAspLeuAspLeu 22
 DB 64 CGTAGTGGGGGAGCAGAGAGACGTCGCGAGCATGCTGGGTGGATTCGACATTCACCTG 123
 QY 23 GluThrGluGluGluGlySerGluGlyGluProGluLeuSerProAlaAspAlaGly 42
 DB 124 GACCAGCCGGAGGACGCGATATCAGACGATGACTGGAG-----GACGGGGCT 171
 QY 43 ProLeuAlaGluLeuArg-----AlaAlaGlyLeuGluProVal 55
 DB 172 ACCTTTATGAGTTCATGACGACCATGGGAGTATCTTATGACATGACATGAG----- 225
 QY 56 GlyHisTyrGluGluValGluLeuThrGluThrSerValAsnValGlyProGluArgTle 75
 DB 226 ---CATTTGTGAAGATTGATGATGACAGATAGTGTGACAAAGATTCACAGAAAGATA 282
 QY 76 GlyProHisCysPheGluLeuLeuArgValLeuGlyLysGlyGlyTyrGlyLysValPhe 95
 DB 283 CGACCAGATGTTTGGACTTCTGCTGTACTGGGGAAGGTGTGTAGGGAAGGTTTTT 342
 QY 96 GluValArgLysValGlnGlyThrAsnLeuGlyLysIleTyrAlaMetLysValLeuArg 115
 DB 343 CAGGTACGGAAGATTAATGGAGCTCATACAGGAAAAATCTTGCAATGAAGTCTTAA 402
 QY 116 LysAlaLysIleValArgAsnAlaLysAspThrAlaHisThrArgAlaGluArgAsnIle 135
 DB 403 AAGGCTATGATTGTACGAATGCTAAAGACACACTCACAATAAGCTGAGAGAAATAT 462
 QY 136 LeuGluSerValLysHisProPheIleValGluLeuAlaTyrAlaPheGlnThrGlyGly 155
 DB 463 TTAGAGAGAGTAAGCATCTTTCATGTGTGATCTTATTATGCTCTTCAACTGTGTGA 522
 QY 156 LysLeuTyrLeuIleLeuGluCysLeuSerGlyGlyLeuLeuPheThrHisLeuGluArg 175

```
Db 523 AAACCTACCTACCTAGATATCTTACCGGAGAGAACTCTTCATGCACTGGAAAGA 582
QY 176 GluGlyIlePheLeuGluAspThrAlaCysPheTyrLeuAlaGluIleThrLeuAlaLeu 195
    |||||.....:|||||.....:|||||.....:|||||.....:|||||
Db 583 GAAGGATATTATGAGAGACACAGCCTTTTATTGGCAGAGATCTCAATGCGCTTAA 642
QY 196 GlyHisLeuHisSerGlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeu 215
    |||||.....:|||||.....:|||||.....:|||||.....:|||||
Db 643 GGACATTTACATCAGAAAGAAATCATTTATCGAGATTGAAACACAGAAACATCATGCTT 702
QY 216 SerSerGlnGlyHisIleLeuLeuThrAspPheGlyLeuCysLysGluSerIleHisGlu 235
    :|||:|||||.....:|||||.....:|||||.....:|||||.....:|||||
Db 703 AATCTTCAGAGGATGTGAACCTTACTGATTTTGGCCTTTGTAAAGAAATCTACATGAT 762
QY 236 GlyAlaValThrHisThrPheCysGlyThrIleGluTyrMetAlaProGluIleLeuVal 255
    ||| |||||.....:|||||.....:|||||.....:|||||.....:|||||
Db 763 GGCACAGTCACACACACTTGTGTGACACATGGAATACATGSCACCGAAATCTTAATG 822
QY 256 ArgSerGlyHisAsnArgAlaValAspTrpSerLeuGlyAlaLeuMetTyrAspMet 275
    |||||.....:|||||.....:|||||.....:|||||.....:|||||
Db 823 AGAAGCGGTCAATACCGCTCTGAGACTGTGAGCGCTGGAGCTTGTATGATGACATG 882
QY 276 LeuThrGlySerProPheProPheThrAlaGluAsnArgLysLysThrMetAspLysIleIle 295
    |||||.....:|||||.....:|||||.....:|||||.....:|||||
Db 883 CTTACTGGAGCACCGCGCTTCTGTGTAAGAAACAGAAAGAAACTATGTATTAATTC 942
QY 296 ArgGlyLysLeuAlaLeuProProTyrLeuThrProAspAlaArgAspLeuValLysLys 315
    :||| |||||.....:|||||.....:|||||.....:|||||.....:|||||
Db 943 AATGTAATTAACCTGCTCCTACCTACCTACCAAGAACGAGATCTGCTTAAGAAAG 1002
QY 316 PheLeuLysArgAsnProSerGlnArgIleGlyGlyProGlyAspAlaAlaAspVal 335
    |||||.....:|||||.....:|||||.....:|||||.....:|||||
Db 1003 CTGCTAAAGAAAGAAATCTCATCTCTGTCGAGCAGAGATTGAGATGCTGAGATGTG 1062
QY 336 GlnArgHisProPhePheArgHisMetAsnTrpAspAspLeuLeuAlaTrpArgValAsp 355
    ||| |||||.....:|||||.....:|||||.....:|||||.....:|||||
Db 1063 CAGGCTCACTCCTTTTTCAGACACATTAATGGAGATATCTTGCTCTGTAAGGTGAA 1122
QY 356 ProProPheArgProCysLeuGlnSerGluGluAspValSerGlnPheAspThrArgPhe 375
    |||||.....:|||||.....:|||||.....:|||||.....:|||||
Db 1123 CCTCCATTTAAACCTCTTTTGAATCTGAAGAGATGTCAGCCAAATTGTGATCAAAAGTTT 1182
QY 376 ThrArgGlnThrProValAspSerProAspAspThrAlaLeuSerGluSerAlaAsnGln 395
    |||||.....:|||||.....:|||||.....:|||||.....:|||||
Db 1183 ACACGACACAGCCCTGTGAGACAGTCCAGATGATGCCACTCAGCGAAAGTGCACACAG 1242
QY 396 AlaPheLeuGlyPheThrTyrValAlaProSerValLeuAspSerIleLysGluGlyPhe 415
    |||||.....:|||||.....:|||||.....:|||||.....:|||||
Db 1243 GGTGTTGTGGGTTTACCTATGTGGCTCCCTCTGTACTTGAAGTGTGAAGAAAGTTT 1302
QY 416 SerPheGlnProLysLeuArgSerProArgArgLeuAsnSerSerProArgValProVal 435
    |||||.....:|||||.....:|||||.....:|||||.....:|||||
Db 1303 TCATTTGAACCAAAATATGCGCTCTCCGCGAGATCATTAAGTGTGTAAGCAACCCGTA 1362
QY 436 SerProLeuLysPheSer----- 441
    |||||.....:|||||.....:|||||.....:|||||.....:|||||
Db 1363 AGCCCTGTGAAGTTTCTCTGAGATATCTGGGCAAGAGGACAGCTGCTGGAACCTCA 1422
QY 442 -----ProPheGlnGlyPheArgProSerProSerLeuProGluProThrGln 457
    ||| |||||.....:|||||.....:|||||.....:|||||.....:|||||
Db 1423 AACACTCAGACACACAGGGAGG---TTTCGAATGAAAGACAGCGGTGTGAAACAAATGAT 1479
QY 458 LeuProLeuProProLeuLeuProProProProProSerThrThrAlaProLeuProIle 477
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1480 GTGACTGTGA-----ACCGGAGAAAGCTTCAGACACCGCTACCAATC 1518
QY 478 Arg 478
    |||
Db 1519 AGA 1521
```